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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 190)
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2 (butledr.L., Arrondel.C., Forestier,L., Cohen-Solal,L., Mollet,G., Gutlerrez.B., Stavrou,C., Gubler,M.C. and Antignac,C.
Structure of the human type IV collagen gene COL4A3 and mutations in autosomal Alport syndrome
J. Am. Soc. Nephrol. 12 (1), 97-106 (2001)
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Schneider,K., Kolthow,S., Schneider,P., Goebel,T., Kaspers,B. and
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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Schneider,K., Kolthow,S., Schneider,P., Goebel,T., Kaspers,B. and
                                                                                                                                                                 Submitted (28-MAR-2000) Antignac C., U423, INSERM, Hopital Necker-Enfants malades 149 rue de Sevres, 75015 Paris, FRANCE
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alpha3 type IV collagen; col4a3 gene.
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972 973 975 976 977 978

981 982 983 984

986 987 988 989

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9991 9994 9995

c 998 c 999 c1000

.534 /gene="BAFF" /codon_start=1

CDS

VERSION KEYWORDS SOURCE

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460 c
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nes 15; Conservative
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/product="TNF family B cell activation factor"
/protein.id="AAM90951.1"
/db_xref="G1:22087371"
/translation="kleGpespasspoteiwdenknerrsivnaestvloaclollad
SKSDIQQKDDSSIVPWLLSFRRGTALEEQGNKIVIKETGYFFIYGQVLYTDTTFAMGH
LIQRKAAHVEGDDLSLYTLFRCIQNMPQSYPNNSCYTAGIAKLEEGDELQLTIPRRRA
KISLDGGGFFFGANRL"
117 c 113 g 164 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-Aug. 2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hrit.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human CDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5'-6 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRI 01-AUG-2002
moderately
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MKPFGVFEDEDELMHRLVLGKLNNLVKEWISDVSESRNLPSVYAVGKIFFTGSY
RLGVHTKGADIDALCVAPRHYERSDFFQSFFEKLKHODGIRNLRAVEDAFVPVIKFEF
DGIEIDLVFARLAIQTISDNLDLRDSSRLRSLDIRCIRSLNGCRVTDEILHLVPNKET
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KWEWPNPVLLKQPEESNLNLPVWDFRVNPSDRYHLMPIITPAYPQQNSTYNVSTSTRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nogai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,K., Takeuchi,K., Arita,M., Nabekura,T., Ishli,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A. Unpublished

2 (bases 1 to 1689)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligo capping; fis (full insert sequence).
Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to
mRNA, clone_lib:HEMBAl clone:HEMBAl006278.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      AKO21867 1689 bp mRNA linear Homo sapiens cDNA FLJ11805 fis, clone HEMBA1006278, similar to POLY(A) POLYMERASE (EC 2.7.7.19).
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HemBal1006278"
/tissue_type="whole embryo, mainly head"
/clone_lib="HEMBAl"
/dev_stage="embryo, 10 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="cloning vector: pME18SFL3" 186. .>1689
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/db_xref="G1:10433147"
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Sus scrofa prophet of pit-1 (Prop-1) mRNA, complete cds.
AF232676
AF232676.1 GI:11275672
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ARDTGLSEARIQVWFQNRRAKQRKQERSLLQPLAHLSPATFSGFLPEPPACPYSYPTP
PPPWTCFPHPYNHALPSQPSTGGSFARHPQSEDWYPTLHPTPTGHLPCPPAPPVLPLS
VMVEEFKQGLAVTDEILQGKSDWSKLLEPPNFFOKYRHYIVLTASASTEENHLEWVGL
VESKIRVLVGNLERNEFITLAHVNPQSFPGNKEHHKDNNYVSWMFLGIIFRRVENAES
VIDLTYDIQSFTDWYFNTMLKEGMKIEATHVKKKQLHHYLPAEIL"
309 c 366 g 459 t
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Submitted (07-FEB-2000) Biology, Indiana University Purdue
University Indianapolis, 723 West Michigan Street, Indianapolis, IN
46202-5132, USA
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Sloop.K.W. McCutchan Schiller,A., Smith,T.P., Blanton,J.R. Jr.,
Robrer,G.A., Meier,B.C. and Rhodes,S.J.
Blochemical and genetic characterization of the porcine Prophet of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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McCutchan Schiller, A.L., Sloop, K.W., Blanton, J.R. Jr., Meier, B.C.
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Mol. Cell. Endocrinol. 168 (1-2), 77-87 (2000)
20519384
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2.1"
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                                                                                                                       Score 15;
Pred. No.
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/db_xref="taxon:9823"
1. .1721
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DVTGTGEGAYMVYFVSFLGTLAVLPGNIVSALLMDKIGRLRMLAGSSWNSCVSCFFLS
FGRSESAMIALLCLFGGVSIASWNALDVLTVELYPSDKRTTAFGFLNALCKLAAVLGI
FITTSFVGTTKAAPLIEASALLAGSSLALKLPETRGOVLO"
8 850 c 810 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be found
        PRI 12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 7 Row: 1 Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                    Strausberg, R.
Direct Submission
Submitted (15-NoV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3190)
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                            gene product, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Similar to KIAA0736 gene product"
/protein_id="AAH00776.1"
/db_xref="G1:12653963"
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             linear
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/clone="IMAGE:3509807"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
          mRNA
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3190 bp
Homo sapiens, Similar to KIAA0736
IMAGE:3509807, mRNA, partial cds.
BC000776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .3190
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                   Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                            BC000776.1 GI:12653962
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Best Local Similarity 100.
Matches 15; Conservative
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                                DEFINITION
                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
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RESULT 6

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/protein_id="AAA49090.1"
//protein_id="AAA49090.1"
//db_xref="G1:511843"
//db_xref="G1:51184"
//db_xref
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FTKPLVITHEGKPEDSSLPKSNVRQPSVFYGLDTLTVVGIAFAAFVIGALLTGALMFI
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VRT 21-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases I to 334).

Barnett,J.V. Moustakas,A., Lin,W., Wang,X.F., Lin,H.Y., Galper,J.B. and Maas,R.L.

Cloning and developmental expression of the chick type II and type III TGF beta receptors

Dev. Dyn. 199 (1), 12-27 (1994)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (library: lambda zap) embryonic brain cDNA to mRNA.
Gallus gallus
CHKTGFBA 3347 bp mRNA linear VRT 21-JUL-
Gallus gallus transforming growth factor-beta type III receptor
                                                                                                                                                                                                                   plasma membrane; transforming growth transforming growth factor-beta type III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="transforming growth factor-beta type III
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AF312211
AF312211.1 GI:15080910
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712 c 708 g 931 t
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1. .3347
/organism="Gallus gallus"
/db_xref="taxon:9031"
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152. 2677
/codon_start=1
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/dev_stage="embryonic"
/germline
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TGF-beta; betaglycan;
                                                                                                                                                                                                                                                                     factor-beta receptor;
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                                                                                                   mRNA, complete CDS
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Query Match
Best Local Similarity
Matches 15; Conserv
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Smith, S.F.
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KWEWPPULLGOPEESNLALD-PWDPRVNPSDRYTHDFI ITPAYPOONSTYNVSTSTRT
VMVEEFROGLAYTDEILGGKSDWSKLLEPPNFPCKRYRYTYLTASASTEENHLEWVGL
VESKIRVLYGNLERNEFTTLAHVNPOSFPGNFRHKDNNYVSMMFLGIIFRRYBNAES
VNIDLTYDIOSTTDTYYRQANNINNLKEGMKIEATHVKKKQLHHYLPAEILOKKKKQS
LSDVNRSGGLGOSKRLSLDSSCLOSSRDTDNGTPFNSPAKSRSDSPSVGETENNSAEPA
AVIVEKRLSVPPAQOLSIPVIGAKVOSTYKTYSPRKNJFHNYDRYTTPHNA
AQGOPHLNGMSNITKTYTFKRSHSFSIDGTFKRLKDVEKFIRLESTFKNDFTAEERKR
                                                                                                                                                                                                                                          Direct Submission
Submitted (09-02T-2000) Surgery Branch, NCI, National Institutes of
Health, Building 10, Room 2847, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="neo-poly(A) polymerase"
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/db_xref="GI:15080911"
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                                                                                 Identification and functional characterization of neo-poly(A) polymerase, an RNA processing enzyme overexpressed in human tumors Mol. Cell. Biol. 21 (16), 5614-5623 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to Homo sapiens poly(A) polymerase protein
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                  1 (bases 1 to 3752)
Topalian, S.L., Kaneko, S., Gonzales, M.I., Bond, G.L., Ward, Y. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ohara,O., Suyama,M., Nagase,T., Ishikawa,K. and Kikuno,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%; Score 15; DB 9; Length 3752; Similarity 100.0%; Pred. No. 39; 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                             2 (bases 1 to 3752)
Topalian, S.L., Gonzales, M.I., Wang, X. and Wang, R.-F.
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232. .2442
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DNA Res. 5 (5), 277-286 (1998)
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Homo sapiens
                                                               Manley, J.L.
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Matches 15; Conser
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ACCESSION
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                                                                                                                            JOURNAL
MEDLINE
                                                                                                                                                                                                                  AUTHORS
TITLE
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MEDLINE
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                                          AUTHORS
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AB018279
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                                                                                    TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFVLVCAFPSVFAIGALTTQPESPRFFLENGKHDEAMMVLKQVHDTNMRAKGHPERVF
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Fugu rubripes cosmid 092H06 genomic DNA fragment, toplalpha gene.
AL035357
Direct Submission
Submitted (08-OCT-1998) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGVWFTMSFSYYGLTVWFPDMIRHLQAVDYASRTKVFPGERVEHVTFNFTLENQIHRG
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1 (bases 1 to 11001)
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Led (01-FEB-1999) Smith S.F., Fugu Group, UK HGMP Resource
Wallcome Genome Campus, Hinxton Hall, Hinxton,
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                                                                                                                                                                                                                                                                                        /tissue_type="brain"
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Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="KIAA0736 protein"
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2 (bases 1 to 11001)
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100.0%;
                                                                                                                                                                                                                                                                          /sex="male"
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Takifugu rubripes
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intronexon	intron	exon intron	exon	intron exon	intron	intron	exon	יוורנסוו	exon	exon	intron	exon	intron exon	intron	exou	intron	intron
333" 106" 20922116,318732	40374092,42044308,43944487,45724654,47304845, 49305051,51255247,53245511,61596303,64006543, 66636848,70637131,72287342,74607587,76937787, 79738122,8912>9014)	/gene="copialpna" join(1812. 1844,2092. 2116,3187. 3283,3527. 3653, 4037. 4092,4204. 4308,4394. 4487,4572. 4654,4730. 4845, 4930. 5051,5125. 5247,5324. 5511,6159. 6303,6400. 6543, 6663. 6848,7063. 7131,7228. 7342,7460. 7587,7693. 7787,	9014) srase I alpha"	/protein_id="CAAZ3015.1" /db_xref="61:15723144" /translation="MSGEHGUSQVKPGSKGSDTHKHKEKHKDKEYRHKDYKKDKER BERKHNNSEHKDHSEKRNRDNERLKHTDSSSEKHREKHKDKERRREEKVKSSLIAK PKKEKENGYYRDLSPAAIKNEPEEDNGIYSSPOHNKTSRRECDDFFFDCKPKKVYFFH	DKKSKKRRHEYEEEDEEEEDIKPKKKKKNNVTEGKKSKKDEEKWKWEEERSTDGSK WRPLEHKGPVFAPPTELDENVKEYYDGKLMKLAAPAEFVATFEAKMLDHEYTTKDVF RKNFFKDWRKEMTSEEKSKITDLNKCNFAGNDYFKAQSEARKOMSKEEKGKIKEDNE RLOEYGFCIMDHKERIGNFRIEPPGLFRGRODHPKWGMLKRRIRPEDIIINGSKDS KHPKPPPGTKWKEVRHDNKYTWLASWTENIQGSIKYIMLNSSRIKGEKOMQKYETAR	RIAKCUDRITRUOYREDWRSKEMRITRORAVALYFIDKLALRAGNEKEEGETAÖTVGCCS LRVEHINLYPKLADGEYVPEPEGKOSTRYNRIP PVEKRYFKNDJE-EDRWGPGDDL FDRLNTSILINKHLOELAMGETARVFRYNRASTTLAQQUKELSCSDDSVPAKILSYNRA NRAVAILCNHQRAPPKTFEKSWQNLQTKIDEKOKQLSAARKQLKAAKABHRASHDDKS KKAVEKRKAVQRITEEQLAMKLQVQATDEEBENKQIALGAAKABHRASHDDKS PFRIY NKYOPRYERAMAT DAMARCAFE	<pre><1812. 1844 /gene="toplalpha" /number=1</pre>	1845 2091 /gene="toplalpha" /number=1	20922116 /gene="toplalpha" /number=202	21173186 /gene="toplalpha" /number=202 31873283	/gene="toplalpha" /numborr=3 3284. 3526 /gene="toplalpha"	/number=3 3527. 3653 /gene="toplalpha"	364. 4036 /gene="toplalpha" /number=4	403/ 4092 /gene="toplalpha" /number=5 4093 4203 /gene="toplalpha"	/number=5 42044308 /gene="toplalpha"	/number=6 43094393 /gene="toplalpha" /number=6	43944487 /gene="toplalpha" /number=7
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us-09-750-609-10.oligo.rge

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VQQISTTDEVLNNPANIFVAQFFGDPPINILEGEGRGDHVDLGDLKIPIPARQGKLQV
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TSKEAYETGFGIDFGAYAVLAVPELEQYVLKGLERHYADAKRATEIVSSQRYKLITTG
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KEVEEVIFGSTLQGGMGQNLSRYAALLAGLPVEVSAYTVNRVCSSGMQAIIEAYREIA
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PYEKLNVFGGAIALGHPLGASGARIVTTLISVLRNKGGRRGIAALCHGTGGGTAIALE
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Eavyrlntaeeilktiegdvvlfdigdgfrlpdryvvldhhgvsdpaeepssvigvsla
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AVFDLKKPPEEVRGFFGEVVDIVITRVKKNIHKLTPPAYPDITPARRN"
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SLARVFLKKEGVKLFQNGVRIK"
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                                                                                                                                                                                                                                                                                                                                   /note= Fatty acid and phospholipid metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="acetyl-CoA C-acetyltransferase"
/protein_id="AAL63334.1"
/db_xref="GI:18159946"
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/protein_id="AAL63337.1"
/db_xref="GI:18159949"
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/protein_id="AAL63336.1"
/db_xref="GI:18159948"
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                                                                                                                                                                                                                                                               /gene="PAE1220"
complement(1424. .2608)
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/gene="PAE1222"
complement(2652. .3722)
/gene="PAE1222"
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4887, 5270
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/gene="PAE1223"
3779. .4897
/gene="PAE1223"
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/gene="PAE1224"
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1 (bases 1 to 11896)
Fitz-Gibbon,S.T., Ladner,H., Kim,U.J., Stetter,K.O., Simon,M.I. and
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Pyrobaculum aerophilum strain IM2 section 65 of 201 of the complete
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Tlypllsyleaeglifaresyvgrrrkiyaltaagebhlaklmddeffrsiiomleg
Ggregdllaavrdelvyidevfdeiegndaeylkemlallkrleekvearlkkalgg"
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Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
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/gene="PAE1219"
complement(601. .1404)
/gene="PAE1219"
/note="PAE1219"
/note="Blosynthesis of cofactors, prosthetic groups, and carriers; Pyridine nucleotides"
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University of California, Los Angeles, 405 Hilgard Ave, Los
Angeles, Ca 90095-1489, USA
1. .11896
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/strain="IM2"
/db_xref="taxon:1373"
complement(129. .608)
/gene="PAE1218"
complement(129. .608)
/gene="PAE1218"
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/db_xref="GI:18159944"
                                                                                                             8123. .8911
/gene="toplalpha"
/number=20
8912. .>9014
/gene="toplalpha"
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                   /number=19
7973. .8122
/gene="toplalpha"
/gene="toplalpha
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VRL 23-AUG-2001

linear

no DNA stage; Flaviviridae;

Baroth, M.

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Avalos-Ramirez, R., Orlich, M., Thiel, H.-J. and Becher, P. Complete genomic sequences of pestiviruses from giraffe and reindeer: evidence for the presence of two novel species within the genus pestivirus
PPYYTPWAEVFNINPVFIGTEWERKIYCALHRLMSPGDILYVEYVDDRETFIALOKGE
APEATRLGALLRKCGFKIVKNWYHPEGGLEGGMKLQAVKV"
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Avalos Ramirez,R., Orlich,M., Thiel,H.J. and Becher,P.
Evidence for the presence of two novel pestivirus species
Virology 286 (2), 456-465 (2001)
                                                                                                                                                                                                                                                           100.0%; Score 15; DB 1; Length 11896; 100.0%; Pred. No. 35;
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/db_xref="taxon:119222"
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/organism="pestivirus giraffe-1 H138"
/isolate="giraffe-1 H138"
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Thiel,H.J.
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Pestivirus giraffe-1 H138 complete genome.
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pestivirus giraffe-1 H138
Viruses; ssRNA positive-strand viruses,
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/db_xref="G1:15282442"
                                                                    complement(8779..9000)
/gene="PAE1236"
complement(8779..9000)
/gene="PAE1236"
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1 (bases 1 to 12602)
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DB 14; 35; ó;

100.0%; Score 15; DE 100.0%; Pred. No. 35; ive 0; Mismatches

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1 CCTTCTCCCCCTGTT | Similarity | 15; Conser

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                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (28-JAN-1993) G. Grandi, Eniricerche, Via F Maritano 26, 2007, S Donato Milanese (MI), ITALY
20097, S Donato Milanese (MI), ITALY
2 (bases I todriguez, F., de Ferra, F., Grandi, G., Perego, M., Venema, G. and van Sinderen, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence and analysis of the genetic locus responsible for surfactin synthesis in Bacillus subtilis
93360813
8355609
                                                                                                           32802 bp DNA linear BCT 1(
B.subtilis srfA-sfp gene region for surfactin synthetase.
X70356 X70357 X70358 X70359
X70356.1 GI:396480
Surfactin synthetase.
Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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1. .10767
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Grandi, G.
                   10245
                                                                                                                                                                                                                                                                                             Bacillus subtilis.
Bacillus subtilis
source
                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                      ORGANISM
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JOURNAL
                                                                                                                            BSSRFAP/C
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KEYWORDS
SOURCE
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gene CDS

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gene CDS

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AEDVKAHLKKQLPAYMVPQTFTFLDELPLTTNGKVNKRLLPKPDQDQLAEEWIGPRNE

1 CCTTCTCCCCCTGTT 15

Qγ

Louis

HTG.

KEYWORDS

SOURCE

ACCESSION VERSION

ORGANISM

AUTHORS TITLE

JOURNAL MEDLINE PUBMED REFERENCE

REFERENCE

AUTHORS TITLE JOURNAL

TITLE JOURNAL

REFERENCE

AUTHORS

AUTHORS TITLE JOURNAL

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TITLE JOURNAL

AUTHORS

REFERENCE

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

AC107069/c LOCUS DEFINITION

RESULT 13

g

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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa.K., Woon,P.Y., Zhao,B., Frengen,E. Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: pBACC3.6
                                                                                                                                                                                                                                                                                                                                            NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-495023, 2000 bp overlap;
The clone sequenced to the right is RP11-563C6, 2000 bp overlap.
Actual start of this clone is at base position 126621 of
RP11-495023.
McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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4372. .4459
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                                                                                                                               AC107069 34578 bp DNA linear PRI 29-MAY-2002
Homo sapiens BAC clone RP11-249A8 from 2, complete sequence.
AC107069
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Submitted (04-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
5 (bases 1 to 34578)
Waterston, R. H.
Direct Submission
Submitted (13-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
6 (bases 1 to 34578)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (29-MAY-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Apr 13, 2002 this sequence version replaced gi:19924179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (15-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 34578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scott, K., Kozlowicz, A., Spalding, L. and Trani, L.
The sequence of Homo sapiens BAC clone RP11-249A8
Unpublished (2001)
3 (bases 1 to 34578)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: H_NH0249A08
                                                                                                                                                                                                                                                                                                                                                                                             Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                  AC107069.5 GI:20146820
                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 34578)
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29177 CCTTCTCCCCCTGTT 29163
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/rpt_family="Alu" 12214. .12509 /rpt_family="L2"

repeat_region repeat_region

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D.

restriction digest.

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Direct Submission

Direct Submission

Direct Submission

Submitted (21-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jun 8, 2000 this sequence version replaced gi:8247412.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations to annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences untogether with a note of the overlapping clone, as we submit sequences with variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

During Sequence is an befound at the following abbreviations are used to associate primary accession on the WORMPED database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 6, constructed by the Sanger Centre Chromosome 6, constructed by the Sanger Centre Chromosome 6, may any acception on the WORMPED is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further MEPIN/Www.sanger.ac.uk/MED/Chro

FRPI-310P17 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further MEPINFAMT: This sequence is not the entire insert of clone RPI-310P17 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RPI-310P17 is at 1310P17 is at 1310P17 is at 1310P17 is at 1310P17 is
       Human DNA sequence from clone RP1-310P17 on chromosome 6. Contains
                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Aluy repeat: matches 158. .308 of consensus"
2432. .2878
/note="LiMB8 repeat: matches 5429. .5879 of consensus"
2879. .3641
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'note="LIMBB repeat: matches 5874. .5991 of consensus"
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//clone_lib="RPCI-1"
132. 426
/note="Alusq repeat: matches 1. .295 of consensus"
complement(428. .891)
/note="match: GSS: Em:B53078"
complement(580. .878)
/note="match: GSS: Em:AQ269829"
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//note="LTR17 repeat: matches 1. .780 of consensus"
3516. .4013
/note="match: GSS: Em:AQ112069"
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/db_xref="taxon:9606"
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                            GSSs, complete sequence.
AL138734
                                                                        AL138734.6 GI:8388469
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2035. 22201
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20561. .20610
/rpt_family="AT_rich"
21029. .21147
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12467. .22528
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9992. .20085
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00002. .20087
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0106, 20441
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24482. 24768
/rpt_family="tl"
25359. 25381
/rpt_family="AT_rich"
26336. 26845
                  'rpt_family="GA-rich"
2723. .12743
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2930. .12965
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1061. .24481
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29081. .29460
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3468. .13770
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18201. .18343
/rpt_family="CR1"
18517. .18822
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4609. .14696
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/rpt_family="Alu"
23765. .23897
/rpt_family="L1"
23988. .24016
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0451. .20530
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:4255. .14316
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'rpt_family="MIR"
.5519. .15572
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5951. .15997
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22922. .23217
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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AL138734/c
LOCUS
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misc_feature

PRI 16-AUG-2000

linear

DNA

43347 bp

AL138734

Op ò

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/note="MIR repeat: matches 59. .145 of consensus" 9753. .9893 /note="All repeat: matches 168. .311 of consensus" 10697. .11158 /note="L2 repeat: matches 2290. .2750 of consensus" 11255. .11286 /note="L6 copies 2 mer ac 100% conserved" 11352. .11558 /note="HERVL repeat: matches 1757. .1969 of consensus" 12998. .13299 /note="HERVL repeat: matches 1757. .1969 of consensus" 14905. .14200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15481. .15498
//note="allus repeat: matches 152. .170 of consensus" 15499. .15731
//note="allus repeat: matches 71. .308 of consensus" 15732. .15790
//note="allus repeat: matches 1. .152 of consensus" 15822. .16105
//note="allus repeat: matches 5830. .6110 of consensus" 16106. .16416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Alusp repeat: matches 1. 313 of consensus"
16417. 17711
/note="LiPah6 repeat: matches 4517. 5830 of consensus"
17737. 18032
/note="MER61A repeat: matches 7. 314 of consensus"
18038. 18426
/note="LiPah6 repeat: matches 4125. 4510 of consensus"
1827. 18706
/note="Lipah6 repeat: matches 3826. 4124 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"MIR repeat: matches 1. .208 of consensus"
14674. .14748
15052. .15480
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/note="1,1MD2 repeat: matches 5774. .6331 of consensus"
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21140. .21264
                        .5429 of consensus'
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/note="LiM4 repeat: matches 3375. .3822 of consensus"
[5481. .15498
                                                                                                                                                                                                                                                 /note="12 repeat: matches 2580. .2750 of consensus" 6304. .6577
/note="Alusx repeat: matches 9. .282 of consensus" 6589. .6721
/note="Alusq/x repeat: matches 1. .133 of consensus"
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//note="L2 repeat: matches 1452. .2147 of consensus"

19893. .19948
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20944. .21113
                                                                                                                                                                                                                                                                                                                                                                                        notes"AluSp repeat: matches 1. .305 of consensus"
164. .7253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluJo repeat: matches 2. .289 of consensus"
8711. .8799
/note="MIR repeat: matches 59. .145 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 47. .147 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7584. 7643
/note="30 copies 2 mer gt 96% conserved"
7969. 8079
/note="MR repeat: matches 28. .143 of consensus"
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                        'note="L1MB8 repeat: matches 5147.
                                                                               ....purpment(4129. .4662)
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4657. .5169
                                                                   /note="match: GSS: Em:AQ508138"
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5449. .5596
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22504. .22755
7 (note="match: GSS: Em:AQ357726"
22608. .22697
7 (note="match: GSS: Em:AQ357726"
7 (note="L2 repeat: matches 2620. .2710 of consensus"
7 (note="L2 repeat: matches 2620. .2710 of consensus"
7 (note="L2 repeat: matches 413. .509 of consensus"
8 (note="LTR22 repeat: matches 38. .312 of consensus"
8 (note="L2 repeat: matches 2005. .2146 of consensus"
8 (note="L2 repeat: matches 2005. .2146 of consensus"
8 (note="L1 repeat: matches 2105. .2146 of consensus"
8 (note="L1 repeat: matches 2105. .2146 of consensus"
8 (note="L1 repeat: matches 2151. .3045 of consensus"
8 (note="L1 repeat: matches 2151. .3045 of consensus"
8 (note="L1 repeat: matches 2151. .3045 of consensus"
8 (note="match: GSS: Em:AQ225006"
8 (note="match: GSS: Em:AQ225006"
8 (note="match: RSA)
8 (note="match: repeat: matches 7250. .7739 of consensus"
8 (note="match: RTA)
8 (note="match: matches 6. .390 of consensus"
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Human DNA sequence from clone RP11-17G2 on chromosome 10, complete
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/note="Cheshire repeat: matches 723. .2420 of consensus"
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/note="MIR repeat: matches 6. .260 of consensus" 3434. .34535
/note="L2 repeat: matches 2574. .2687 of consensus" 34633. .35136
/note="Alusc repeat: matches 1. .125 of consensus"
21581. .21650
21747. .21850
21747. .21805. .22281)
//note="LiMD3 repeat: matches 7476. .7579 of consensus"
complement(21823. .22281)
//note="match: GSS: Em:AQ714858"
22304. .22755
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/note="Cheshire repeat: matches 27. .548 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="LTRL6C repeat: matches 102. .387 of consensus" 32151. .32455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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/note="match: GSS: Em:AQ735362"
31390, .31669
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AL583852.6 GI:14702147
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Matches 15; Conservative
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Submitted (03-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On or before Jul 12, 2001 this sequence version replaced
gi.7381811, gi:13396759.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
this sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were ocvered by at least
one plasmid subclone or more than one M13 subclone; and the
absembly was confirmed by restriction digest. The following
absembly was confirmed by restriction digest. The following
absembly was re used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw.;
SWISSPROT: Tr:, TREMBL; Wp:, MORMPEP; Information on the WORMPEP
then the feature table with their source databases: Em:, EMBL; Sw.;
SWISSPROT: Tr:, TREMBL; Wp:, MORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
RP11-17G2 is from the library RPCI-11.1 constructed by the group of bleter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPORTANT: This sequence is not the entire insert of clone RP11-17G2 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-17G2 is at 56701 in this sequence. The true right end of clone RP11-397115 is at 2000 in this
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 56701)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
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/note="MIR repeat: matches 45. .258
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note="MER1B repeat: matches 1.
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note="match: GSS: Em:AQ812738"
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/note="match: GSS: Em:AQ475942"
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/note="MIR repeat: matches 61.
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1. .56701
/organism="Homo sapiens"
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/clone_lib="RPCI-11.1"
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/chromosome="10"
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JOURNAL
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                                                                                                       AUTHORS
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/note="MLT1A1 repeat: matches 337. .568 of consensus" 9753. .10220
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26933, .27097
                                                                                                                                                                                                                             /note="L2 repeat: matches 2284, .2534 of consensus"
8947. .9112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.70te="MER46C repeat: matches 7. .338 of consensus" 18670. .18785 repeat: matches 45. .163 of consensus" 18833. .19044 repeat: matches 28. .260 of consensus" 7.0te="MIR repeat: matches 28. .260 of consensus" 21936. .21145 repeat: matches 5599. .5820 of consensus 22148. .22199
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//note="MIR repeat: matches 87. .165 of consensus" 22950

//note="MER3 repeat: matches 1. .200 of consensus" 23508 .23698 / .23698 / .23698 / .23698 / .23448 / .24458 / .24458 / .24458 / .24458 / .24458 / .24581 / .2213 of consensus" 24486 .24581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 2242. .2521 of consensus"
16664. .16777
16042="L2 repeat: matches 2596. .2708 of consensus"
16779. .16842
100te="16 copies 4 mer ggaa 81% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consensus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MER5A repeat: matches 18. .178 of consensus"
16288. .16546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2318 of consensus"
                                                                           /note="MER91A repeat: matches 5. .95 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER5A repeat: matches 1. .188 of consensus" 27101. .27219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MLTIF repeat: matches 1. .371 of consensus" complement(25325. .25729)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // Anotes 13 copies 4 mer caca 82% conserved 22199. .22596 // Anotes 1. .426 of consensus 22480. .22743 // Anotes match: STS: Em:HS094YH3" // Anotes match: STS: Em:HS094YH3" // Anotes 22599. .22638 // Anotes 22599 // Anote
                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 70. .248 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .214 of consensus"
                                                                                                                                                      .234 of consensus"
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/note="21 copies 4 mer ggaa 75% conserved"

16951. .16994

1700te="11 copies 4 mer ggaa 81% conserved"

17973. .18165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="10 copies 4 mer caca 92% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10458. .10642

/note="L2 repeat: matches 2129. .2318 of

13448. .13763

/note="MLT1A1 repeat: matches 1. .341 of

13847. .13898

/note="2"2 copies 26 mer 94% conserved"
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25073. .25451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16817 .16998
/note="7 copies 26 mer 62% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: GSS: Em:AQ497216"
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18174. .18509
                                                                                                                                                      /note="MIR repeat: matches 9.
GSS: Em: AQ083388"
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/note="MIR repeat: matches 13. .134 of consensus"

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29578. .29664

// note="MIR repeat: matches 82. .175 of consensus" 31386. .31508
// note="MIR repeat: matches 42. .164 of consensus" 31974. .3234
// note="MIR repeat: matches 1. .16 of consensus" 31596. .33015 repeat: matches 1. .410 of consensus" 32596. .33015 repeat: matches 128. .547 of consensus" 3407. .33833. .34015
// note="MIR repeat: matches 50. .251 of consensus" 3122. .34214
// note="MIR repeat: matches 50. .251 of consensus" 3122. .34214
// note="MIR repeat: matches 46. .140 of consensus" 37028. .35190. .35474
// note="MIR repeat: matches 46. .140 of consensus" 37028. .37195
// note="MIR repeat: matches 2137. .2276 of consensus" 3704. .37413
// note="L2 repeat: matches 2137. .2276 of consensus" 37801. .39465
// note="L2 repeat: matches 1655. .2599 of consensus" 38541. .39465
// note="L2 repeat: matches 59. .220 of consensus" 39625. .39782
// note="MIR repeat: matches 59. .220 of consensus" 39625. .39782
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               /note="MIR repeat: matches 49. .103 of consensus" 28697. .28879
/note="MIR repeat: matches 31. .225 of consensus" 29356. .29488
/note="MIRSA repeat: matches 50. .184 of consensus" 29578. .29664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L2_repeat: matches 2517. .2691 of consensus" 41278. .41718
//note="MLT1C repeat: matches 5. .462 of consensus" 41719. .41924
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/note="L2 repeat: matches 2161. .2419 of consensus"
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liver for g

foetal #16586

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ALIGNMENTS
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amphetamine abuse; probe; ss
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Norepinephrine transporter; orthostatic intolerance, gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine;
Probe for human norepinephrine transporter gene A457P variant allele.
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The present sequence represents a probe for the A457P variant allele of a human norepinephrine transporter gene. The specification a method for succeptibility to sub-optimal norepinephrine transport. In a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine reansport in a target cell and treating susceptibility to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, and the form the coaine or the form of the coaine or the form of the for
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                                                                                                                         Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
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                             Robertson D, Blakely RD;
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                        WPI; 2001-425681/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amphetamine abuse.
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AAC09241/c
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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                                                                                                                                                                                                                                                                                                     Score 15; DB 21; Length 352; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                       Sequence 352 BP; 111 A; 73 C; 97 G; 69 T; 2 other;
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 50328.
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                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monahan JE;
                                                                                                                                                                                                                                    expression and secretion vectors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABV50337 standard; cDNA; 445 BP
                                                                                                                                                                                                                                                                                                       100.0%;
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2000US-207454P.
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2000US-219007P.
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nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 149 CCTTCTCCCCCTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                             1 CCTTCTCCCCTGTT 15
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25-MAY-2000;
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                                      cancer in a patient;
assessing the efficacy of a therapy for inhibiting prostate cancer
                                    selecting a composition for inhibiting prostate cancer in a patien assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
                                                                                               assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                          Score 15; DB 23; Length 445; Pred. No. 32;
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                                                                                                                                                                     Sequence 445 BP; 109 A; 118 C; 109 G; 107 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #1856.
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                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                          100.08;
                                                                                                                                                                                                                         100.08;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                     370 CCTTCTCCCCTGTT 384
                                                                                                                                                                                                                                                                                   1 CCTTCTCCCCCTGTT 15
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                                                                                                                                                                                                                           Local Similarity
nes 15; Conserv
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                     in a patient;
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AAH15437;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 [all-length CDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                               Human; primer; detection; diagnosis; antisense therapy; gene therapy;
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Otsuki T;
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                                                                                                                Length 549;
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                                                                                        Sequence 549 BP; 114 A; 178 C; 140 G; 117 T; 0 other;
                                                                                                                100.0%; Score 15; DB 23; 100.0%; Pred. No. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugiyama T, Wakamatsu A, Nagai K,
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                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                      Human cDNA clone (5'-primer) SEQ ID NO:886.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                            Conservative
                                                                                                                                                                                 423 CCTTCTCCCCTGTT 437
                                                                                                                                                                   1 CCTTCTCCCCTGTT 15
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                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                 AAH04051/c
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detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH13142 represent human cDNA sequences; AAB92446 to AAH36593 represent human amino acid sequences; and AAH13629 to AAH13629 represent oligonucleotides, all of which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Otsuki
                                                                                                                                                                                                                                                                               Sequence 827 BP; 264 A; 138 C; 199 G; 223 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 15; DB 22;
100.0%; Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Sugiyama T, Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA sequence SEQ ID NO:13660.
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ID AAH15437 standard; cDNA; 1689 BP.
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2000JP-0183767,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 CCTTCTCCCCCTGTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCTTCTCCCCCTGTT 15
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particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAM13166 to AAM13628 and AAM13633 to AAM18742 represent human cDNA esquences; AAB92446 to AAM195893 represent human amino acid sequences; and AAM13629 to AAM13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a variant norepinephrine transporter. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful for gene therapy for modulating norepinephrine transport in a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine; amphetamine abuse; ss.
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                                                                                                                                                                                                    100.0%; Score 15; DB 22; Length 1689; 100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding human norepinephrine transporter variant A457P.
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                  Sequence 1689 BP; 555 A; 309 C; 366 G; 459 T; 0 other;
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                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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11-JAN-2000; 2000US-0175456.
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                                                                                                                             of the present invention.
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Best Local Similarity
Matches 15; Conserv
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                  function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, hypertension, heart disease, psycho
cell and treating susceptibility to impaired norepinephrine transporter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                            nephrine transporter; orthostatic intolerance; gene therapy; illness; hypertension; heart disease; stimulant abuse; cocaine;
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                                                                                                                                                               Gaps
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                                                                                                                        22; Length 1854;
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                                                                                      Sequence 1854 BP; 356 A; 555 C; 493 G; 450 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding human norepinephrine transporter variant.
                                                     stimulant abuse e.g. cocaine or amphetamine abuse.
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                                                                                                                      100.0%; Score 15; DB
100.0%; Pred. No. 30;
iive 0; Mismatches
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1.1854
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                                                                                                                   Query Match
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amphetamine abuse; ss.
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2000US-0229513
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2000US-0231244
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2000US-0231244
2000US-0231413
2000US-0232081
2000US-023239
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25-SEP-2000;
26-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
                                                                                                  Gaps
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                                         100.0%; Score 15; DB 22; Length 1854; 100.0%; Pred. No. 30;
                                                                                               Indels
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Sequence 1854 BP; 357 A; 554 C; 493 G; 450 T; 0 other;
                                                                                             Mismatches
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2000US-0205515.
2000US-0209467.
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2000US-0225213
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                                                                                                  Conservative
                                                                                                                                                1 CCTTCTCCCCTGTT 15
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Best Local Similarity
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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1 CCTTCTCCCCTGTT 15

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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to
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                                                                2000US-0249212.
2000US-0249213.
2000US-0249214.
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2000US-0249297.
2000US-0249299.
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2000US-0249264.
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2000US-0251030.
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Best Local Similarity 100.
Matches 15; Conservative
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17-NOV-2000;
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17-NOV-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of orientifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity
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from WIPO
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                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #19092.
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                                                                                                                   BP.
                                                                                                   1288/c
AAS83288 standard; cDNA; 2451
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1070 CCTTCTCCCCTGTT 1084
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mes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; nootropic; neuroprotective; antiviral;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 1036.
                                                                                                                                                                                     ABL90474 standard; cDNA; 2520 BP
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164 CCTTCTCCCCCTGTT 150
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P-PSDB; ABB90065.
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                                                                                                              RESULT 11
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acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes, cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                                                                                                                                                                                                 Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder;
                                                                                                                                                                                                                                                   hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
                                                                                                                                                           DNA encoding novel central nervous system protein #584.
ABK44004 standard; cDNA; 2522 BP
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2000US-0189874.
2000US-0190076.
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                                                                                                     05-JUN-2002 (first entry)
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16-MAR-2000;
17-MAR-2000;
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07-JUL-2000;
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22-AUG-2000;
22-AUG-2000;
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11-JUL-2000;
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2000US-0232080.
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2000US-0232399.
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2000US-0236369.
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2000US-0249244
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08-SEP-2000;
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08-SEP-2000;
12-SEP-2000;
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20-OCT-2000;
20-OCT-2000;
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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded to novel central nervous system protein. (I) and polypeptides (III) encoded a pathological condition. Disorders which are diagnosed or treated include autolimmune diseases e.g. rheumatoid arthritis, hyperproliferative cardiasorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease and anjorgenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. captulred immunodeficiency virus (AIDS) and fungl, ocular disorders e.g. dabetes e.g. corneal infection, gastrointestinal disorders e.g. dysphagia.

CC e.g. Acquired immunodeficiency virus (AIDS) and fungl, ocular disorders e.g. dabetes can pitutary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders e.g. nonallergic rhinitis, renal disorders e.g. cespiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. caute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM
                                                                                     2000US-0249300.
2000US-0250160.
2000US-025131.
2000US-0251330.
2000US-0251988.
2000US-0251719.
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2000US-0251868.
2000US-0251869.
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Matches 15; Conservative C
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                                                   2000US-0249297
2000US-0249299
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P-PSDB; AAU87674.
               17-NOV-2000;
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16-JUN-2000 (first entry)

Sequence 3580 BP; 734 A; 942 C; 1024 G; 880 T; 0 other;

g

Human secreted protein clone as180_1 nucleotide sequence SEQ ID NO:159.

antibacterial; antifungal; cytostatic; antiinflammatory; dermatological; antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide; antithyroid; immune deficiency; severe combined immunedeficiency; SCID; infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; secreted protein; immunestimulant; immunesuppressant; virucide; rheumatoid arthritis; autoimmune pulmonary inflammation; asthma; Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis; insulin dependent diabetes mellitus; graft-versus-host-disease; autoimmune inflammatory eye disease; allergy; ss. Human;

Homo sapiens.

WO200009552-A1.

24-FEB-2000

99WO-US18298 13-AUG-1999; 98US-0096622 98US-0096815 98US-0099229 14-AUG-1998 04-SEP-1998 23-OCT-1998

98US-0105368. 99US-0115234. 99US-0119931. 99us-0120575 99US-0132020 08-JAN-1999; 12-FEB-1999; 18-FEB-1999 30-APR-1999

(GEMY) GENETICS INST INC.

99US-0096622

Collins-Racie LA, Evans C; Steininger RJ, Spaulding V; 4, LaVallie ER,
M, Agostino MJ,
Fechtel K; McCoy JM, D, Treacy M Jacobs K, Merberg D. Wong GG,

WPI; 2000-205979/18. P-PSDB; AAY94977 New polynucleotides encoding secreted proteins, which may have e.g. nutritional, chemokine, immune stimulating or suppressing, hematopoiesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor inhibition activity

Claim 168; Page 613-614; 641pp; English.

AAA16618 to AAA16697 encode the human secreted proteins given in AAV84898 to AAV9480 isolated from human adult brain, adult thyroid, adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney, cadult placenta, adult testis, whole embryo, adult cartilage, kidney, foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour, and adult bladder, cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. The polynucleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight chromosomes or to map gene positions. The proteins can be used as chromosome or to map gene positions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined immunedeficiency (SCID), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency virus (HIV), hepatitis, herpesviruses, mycobacteria, Leismania spp., malaria and conditions in the conditions. The proteins can be used to treat autoimmune disorders such as connective tissue disease, multiple sclerosis, systemic lupus erythematosis, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host-disease and autoimmune inflammatory eye disease. The proteins can also be used to treat allergic conditions, such asthma. AAA16698 to AAA16774 represent probes for the human secreted proteins from the present invention.

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                                                                                                                                                                                                                             Human secreted protein; hyperproliferative disorder; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lavallie ER, Collins-Racie LA, Evans C;
Agostino MJ, Bowman MR, Spaulding V, Wong GG;
Howes SH, Resnick RJ, Gulukota K, Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                         Gaps
                        ;
 Length 3580;
                         Indels
                                                                                                                                                                                                       cDNA sequence #21 encoding novel human secreted protein.
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Score 15; DB 21;
Pred. No. 29;
                         Mismatches
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100.0%;
100.0%;
                                                                                                                                 ABK35630 standard; cDNA; 3580
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                                                                                                                                                                                (first entry)
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                                                                      2528 CCTTCTCCCCTGTT 2542
                         Conservative
                                               1 CCTTCTCCCCCTGTT 15
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Clark HF, Fechtel K,
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Merberg D,
                                                                                                                                                         ABK35630;
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The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. severe combined represent immunodeficiency (SCID), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. heampatis), allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis, coagulation disorders (e.g. heampobilia), and tumnours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35610-ABK36232 represente cDNA sequences of the invention that encode for novel human secreted proteins.

Claim 1; Page 85-86; 393pp; English.

Sequence 3580 BP; 880 A; 1024 C; 942 G; 734 T; 0 other;

DB 24; Length 3580; 100.0%; Score 15;

Query Match

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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                      Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.

(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

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                  Gaps
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                  Indels
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red. No. 29;
Mismatches
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 Pred. No.
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2000US-189862P.
2000US-201454P.
2000US-2113144P.
2000US-219007P.
100.08;
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                                                                                                                                                                                                                          13-SEP-2002 (first entry)
                                                               1053 CCTTCTCCCCCTGTT 1039
               Conservative
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25-MAY-2000;
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US-09-356-281-42
US-08-291-932A-763
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Patent No. 5830662

GENERAL INFORMATION:

APPLICANT: The Trustees of Columbia University in the City
APPLICANT: of New York

TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
TITLE OF INVENTION: CDNA LIBRARIES

TUTLE OF INVENTION: CDNA LIBRARIES

VAMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 86.7%; Score 13; DB 4; Length 776; Best Local Similarity 100.0%; Pred. No. 37; Matches 13; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Incyte ID No. 6426186 199069.2CB1
US-09-484-970B-82
US-09-039-641-36
US-09-039-762A-36
US-09-013-612A-36
US-08-446-803-5
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US-09-170-670-15
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US-09-183-412-14
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US-09-245-281-27
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 82, Application US/09484970B
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILIOR DATE: 2000-01-18
CURRENT FILIOR DATE: 2000-01-18
SOFTWARE: PERL Program
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NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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STREET: 405 Lexington Avenue
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TITLE OF INVENTION: An Oral Care Product Comprising A Mutan
Binding Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,744A
FILING DATE: 20-Apr-1999
CLASSIFTCATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                          COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLM PC compatible
COMPUTER: BLM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,542B
FILING DATE: June 21, 1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4735.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.7%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 37; Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 42840-A-PCT-US
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 122-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-295-744A-1

Sequence 1, Application US/09295744A

Patent No. 6355228

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTĒRISTICS:
LENGTH: 1419 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1020 CCTTCTCCCCTG 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCTTCTCCCCTG 13
                   CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Gaps

. 0

Indels

Length 2431;

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GENERAL INFORMATION:
APPLICANT: Allen, Rebecca L.
APPLICANT: LONGAGIe, David M.
TITLE OF INVENTION: A Pollen-Specific Promoter From Maize
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: MADARESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.7%; Score 13; DB 1;
100.0%; Pred. No. 37;
tive 0; Mismatches
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                               Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/07/911,532
FILING DATE: 09-JUL-1992
ATTORNEY AGENT INFORMATION:
NAME: POCHOPIEN, DONAIG J.
RESISTRATION NUMBER: 3167
REFERENCE/DOCKET NUMBER: 92 P139
TELECOMMUNICATION INCREMATION:
                                                                             PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 500 W. Madison, 34th Floor
CITY: Chicago
STATE: 111inis
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08149695
Patent No. 5412085
                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATCHIN Release #
                                                                                                                                                                                           86.7%; 3
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (312)707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2687 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (312)707-9155
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                               NAME/KEY: misc_feature LOCATION: 1...2431
                                                                                                                                                                                           Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                             655 TTCTCCCCTGTT 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
STRAIN: Line W22
                                                                                                                                                                                                                                                                         3 TTCTCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TTCTCCCCTGTT 15
                                       UNKNOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO ORIGINAL SOURCE:
                                       ANTI-SENSE: UNK
ORIGINAL SOURCE:
ORGANISM: POF
 MOLECULE TYPE:
                                                                                                                                   ; LOCATION:
US-09-221-017B-351
                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; STRAIN:
US-08-149-695-8
                                                                                                                                                                                                                                                                                                                                                                                         US-08-149-695-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   86.7%; Score 13; DB 4; Length 1905; 100.0%; Pred. No. 37; ative 0; Mismatches 0; Indels
                                                                                                                               STRAIN: Trichoderma harzianum CBS 243.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Windows
SOFTWARE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PC27AU98/01023
FILING DATE: 10-DEC-1998
ATORNEY/AGENT INFORMATION:
NAME: MOILOY, Gladys H
REFERENCE/DOCKET NUMBER: 27340-20021.00
                                                                                                                                                                   NAME/KEY: sig_peptide

LOCATION: 1..120
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-295-744A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 351, Application US/09221017B Patent No. 6444799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
                 LENGTH: 1905 base pairs
                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 351:
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                     1568 CTTCTCCCCTGT 1580
                                                                                                                                                                                                                                                                                                                                               2 CTTCTCCCCCTGT 14
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                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 13; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-221-017B-351/c
                                                                                                                                                 FEATURE
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Gaps

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Indels

Length 2687;

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86.7%; Score 13; DB 1; Length 2873; 100.0%; Pred. No. 37; tive 0; Mismatches 0; Indels
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Patent No. 5545546
GENERAL INFORMATION:
APPLICANT: ALLEN, Rebecca L.
APPLICANT: LONSDALE, David M.
TITLE OF INVENTION: A Pollen-Specific Promoter From Maize NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNDER: US/07/911,532
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: POchopien, Donald J.
REGISTRATION NUMBER: 92 P139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)707-8889
TELEFAX: (312)707-8889
TELEFAX: (312)707-9155
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-JAN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/149,695
                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/377,228
FILING DATE: 24-JAN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             663 TICICCCCTGIT 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea ma
STRAIN: Line W22
TISSUE TYPE: Pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                              FILING DATE:
                                                       60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-149-695-1
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                                                                                                                     Sequence 8. Application US/08377228

Patent No. 5545546

GENERAL INFORMATION:
APPLICANT: ALLEN, Rebecca L.
APPLICANT: ALLEN, Rebecca L.
TITLE OF INVENTION: A Pollen-Specific Promoter From Maize
UNDMERS OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foldy & Lardher
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Allen, Rebecca L.
APPLICANT: Allen, Rebecca L.
APPLICANT: Lonsdale, David M.
TITLE OF INVENTION: A Pollen-Specific Promoter From Maize NUMBER OF SQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held and Malloy
STREET: 500 W. Madison, 34th Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY: USA
ZIP: 20007-5109
COUNTY: USA
ZIP: 20007-5109
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,228
FLING APPLICATION DATA:
APPLICATION NUMBER: US/08/377,228
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/149,695
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/911,532
FILING DATE: 09-UUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
RESISTENCE/DOCKET NUMBER: 33229/290/PIHI
TELECOMMUNICATION NUMBER: 33239/290/PIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.7%; Score 13; DB 1; 100.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 37; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08149695
Patent No. 5412085
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2687 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
477 TTCTCCCCTGTT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 TTCTCCCCTGTT 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                      RESULT 6
US-08-377-228-8
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                qq
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Gaps

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Sequence 53, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENES
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                  Length 4287;
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                                                                                                                                                                                                        Indels
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                                                                                                                                                                DB 1;
36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.7%; Score 13; DB 1;
100.0%; Pred. No. 36;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                  Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CTASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFRAX: (215) 568-5549
                                                                                                                                                                                                      0;
                                                                                                                                                              86.7%; :
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                               Homo sapiens
                                                                                                                                                        Ouery Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: NO. 5734039e INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
                                                                                  CDS
1579..3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                298 TICICCCCTGIT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 TICICCCCTGII 286
                                                                                                                                                                                                                                             3 TICICCCCCTGIT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Penn Ce
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TTCTCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                    ORIGINAL SOURCE:
ORGANISM: HOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                            US-08-306-691B-53/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-08-770-301A-2/C
                                                                                ; NAME/KEY:
; LOCATION:
US-08-244-189-1
      ANTI-SENSE:
                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                             Óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
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0
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APPLICANT: Kikuchi, Kimiko
APPLICANT: Kikuchi, Kimiko
APPLICANT: Miyoshi, Hiroyuki
APPLICANT: Miyoshi, Hiroyuki
APPLICANT: Kozu, Tomoko
TITLE OF INVENTION: No. 5580727el DNAs, Polypeptides Encoded Thereby
TITLE OF INVENTION: and Methods for Detecting the DNAs and Polypeptides
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                 86.7%; Score 13; DB 1; Length 2873; 100.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/244,189
FILING DATE: 15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 37;
0; Mismatches
                                                                                              NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 33229/290/PIHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                         US 07/911,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           760-183P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-08-244-189-1/c
; Sequence 1, Application US/08244189
; Patent No. 5580727
; GENERAL INFORMATION:
APPLICANT: Ohki, Misao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY MEDIT INFORMATION:
NAME: MUTPHY JE., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2873 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 7.
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 205-8000
(703) 205-8050
FILING DATE: 09-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                           FILING DATE: 09-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 4287 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 8110 Gatehou
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      663 TTCTCCCCTGTT 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TTCTCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                          linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22042
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ADDRESSEE: No. 63552280 No. 6355228disk of No. 6355228th America, Inc. STREET: 405 Lexington Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09295744A
Patent No. 635528
GENERAL INFORMATION:
APPLICANT: Fuglsang, Claus Crone
TITLE OF INVENTION: An Oral Care Product Comprising A Mutan
Binding Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13; DB 3; Length 4503;
Pred. No. 36;
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/175,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ_for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,993
REGISTRATION NUMBER: 4735.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,744A
FILLING DATE: 20-APP-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,301
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1422-287
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-205-8000
TELEFAX: (703)-205-8050
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; P.
Matches 13; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 4503 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
; IDENTIFICATION METHOD:
US-09-175-581-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2923 CCTTCTCCCCCTG 2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CCTTCTCCCCCTG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA ZIP: 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NY
                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-295-744A-12
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                                                     APPLICANT: IKEDA, JUN
APPLICANT: KANEDA, SUMIKO
APPLICANT: KANEDA, SUMIKO
APPLICANT: YANGGI, HIDEKI
APPLICANT: YURA, TAKASHI
TITLE OF INVENTION: NOVEL STRESS PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CHTY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Sequence 2, Application US/09175581

Sequence 2, Application US/09175581

GENERAL NO. 6034222

GENERAL INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: KANEDA, SUMIKO
APPLICANT: YANAGI HIDEKI
APPLICANT: YUNAGI HIDEKI
APPLICANT: YUNAGI HIDEKI
APPLICANT: WUNAGI HIDEKI
APPLICANT: WONGI STRESS PROTEINS
NUMBER OF INVENTION: NOVEL STRESS PROTEINS
NUMBER: OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747

COTTY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.7%; Scc. 100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/770,301A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
Sequence 2, Application US/08770301A Patent No. 5948637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURENT UR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1422
TELECOMUNICATION INFORMATION:
TELECHONE: (703)-205-8000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4503 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2923 CCTTCTCCCCTG 2911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-770-301A-2
                                                                                                                                                                                                                                                                                             STATE:
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TELEFAX: 212-878-96: INFORMATION FOR SEQ ID NO: 12

COUNTRY: USA ZIP: 22040-0747

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US-09-103-840A-1
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Patent No. 645294

BREERAL INFORMATION:
APPLICANT: GAN, Weinlu et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO01173

CURRENT APPLICATION NUMBER: US/09/813,133A

CURRENT PILLOSTE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO01073

CURRENT FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 55827
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37RV
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                                                                                                                                                                                                                                                                                                                Length 6032;
                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                      STRAIN: Trichoderma harzianum CBS 243.71
                                                                                                                                                                                                                                                                                                            86.7%; Score 13; DB 4;
100.0%; Pred. No. 36;
tive 0; Mismatches
                                                                                                                                                                                               NAME/KEY: CDS

LOCATION: 3188..5092

US-09-295-744A-12
                       LENGTH: 6032 base pairs
                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 13; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-813-133A-3/C
                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-103-840A-1
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6, Appî 42, App 9, Appl

Appli 9, App App1i

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12763, A
17945, A
29686, A
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20180, AP
20116, AP
20116, AP
68887, AP
1002, AP
11002, AP
11002, AP
11025, AP
2017, AP
2017,
                                                                                                                                                                                                                                                                                                          93, Appi
479, App
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-880-107-3234/c
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Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
    Sequence 195, App Sequence 301, Ap Sequence 301, Ap Sequence 2604, Ap Sequence 2604, Ap Sequence 4427, Ap Sequence 18515, A Sequence 199, App Sequence 133, App Sequence 27, Appl Sequence 27, Appl Sequence 104, App Sequence 104, App Sequence 104, App Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 11, Appl Sequence 543, App Sequence 3114, App
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
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US-09-880-107-195
US-09-24-093B-3446
US-09-264-093B-3446
US-09-764-877-2603
US-09-764-877-2604
US-09-864-761-18515
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US-09-956-119
US-09-96-119
US-09-96-788-323
US-09-96-788-323
US-09-96-788-323
US-09-96-788-323
US-09-96-788-323
US-09-96-788-26
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0 US-09-965-099-6
1 US-09-985-08-107-11
0 US-09-974-300-2126
0 US-09-976-983-947
0 US-09-965-198-16
0 US-09-865-198-16
0 US-09-865-198-16
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US-09-960-352-4630
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Best Local Similarity 100.
Matches 15; Conservative
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  RESULT 2
US-09-954-456-1577/c
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US-09-764-864-1704
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LENGTH: 15857
  TYPE: DNA
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Patent No. US20020142981A1
Sether No. US20020142981A1
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uscherf, Usche
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FILE KREEKENLE: 092-30.70
CURRENT PAPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR PILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DAT
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: LOCATION: (1)..(389)

: OTHER INFORMATION: n = a or c or g

US-09-880-107-3234
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; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-1577
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1992
LENGTH: 8894
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CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
CTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
US-09-864-761-13104
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT23
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEO ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SED ID NO 13104
LENGTH: 594
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
                          FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
                                                                         PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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US-09-764-864-1692
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OTHER INFORMATION:
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US-09-764-864-1692/C
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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Profile REFERENCE: DEX-0277
CURRENT APPLICATION NUMBER: 00749,997
PRIOR PILIG DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: Patentin version 3.1
SEQ ID NO 84
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hone, Wensheng
TITLE OF INVENTION: BENEBERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: 105/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-20-4
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
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93.3%; Score 14; DB 10; Length 389;
100.0%; Pred. No. 15;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 14;
....ve 0; Mismatches
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PRIOR PLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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                                                 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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APPLICANT: Salceda, Susana
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296 CCTTCTCCCCTGT 283
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; ORGANISM: Homo sapien
US-10-001-835-84
                          Best Local Similarity
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US-10-001-835-84/c
  Query Match
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-922-217-616/c
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Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: ADOI-05-23
PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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                  Sequence 3063, Application US/09764877
Fatent No. US20020147140a1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper, NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3063
LENGTH: 8894
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Patent No. US20020147140a1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FIER REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3349

LENGTH: 16877
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                              TYPE: DNA
GORGANISM: Homo sapiens
US-09-764-877-3063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-764-877-3349
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Matches 14; Conserv
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US-09-764-877-3349/C
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US-09-764-877-3063
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## PRIOR FILING DATE: 0000-09-12 66/236,356
## PRIOR FILING DATE: 0000-09-12 66/236,356
## PRIOR FILING DATE: 1001-01-30
## PRIOR PRIOR PAPELICATION WINNERS: PST/US01/0066
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DETERMINING THE FUNCTIONS AND
INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
                                    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: CAMPOSITIONS SOF OVARIAN CANCER FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 4769
LENGTH: 285
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100.0%; Pred. No. 52;
iive 0; Mismatches
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PRIOR PELICATION NUMBER: PCT/USGO//02246
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/118,206, PRIOR PELING DATE: 1999-03-26
PRIOR PELING DATE: 1999-03-26
PRIOR PELING DATE: 1999-03-26
PRIOR PILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FASTERE OF WINDOWS VERSION 4.0
SEQ ID NO 96
LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Eisenberg, David
APPLICANT: Eisenberg, Sergio H.
APPLICANT: ROLSTEIN, Sergio H.
APPLICANT: MARCOLLE, Edward M.
TITLE OF INVENTION: DITERALISING THE FUNCTI
TITLE OF INVENTION: INTERACTIONS OF PROFE
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
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; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 96, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:
                Harlocker, Susan L.
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-09-867-701-4769
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US-09-867-701-10110/c
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APPLICANT: Wang, Aijun

APPLICANT: Clapper, John A.

APPLICANT: Meagher, Madeleine J.

APPLICANT: Meagher, Madeleine J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: COMPOUNDS FOR 
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                                                                                             APPLICANT: Wang, Allun
APPLICANT: Wang, Allun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
TITLE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
SOFTWAREN FILING DATE: 2001-08-03
SOFTWARES: FastSEQ for Windows Version 4.0
SEQ ID NO 616
LENGTH: 210
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Patent No. US2002013237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LCCATION: 156, 181, 194
; OTHER INFORMATION: n = A,T,C or G
US-09-922-217-616
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NAME/KEY: misc_feature

LOCATION: (1)...(210)

OTHER INFORMATION: n = A,T,C or G
Jiang, Yuqiu
Smith, Carole Lynn
King, Gordon E.
Wang, Aijun
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Best Local Similarity 100.
Matches 13; Conservative
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Matches 13; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCTTCTCCCCTG 13
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ORGANISM: Homo sapien
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Fatent No. US20020115057A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

FAPLICANT: Young, Paul

TITLE OF INVERMION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVERMION: Process for Identifying Anti-Cancer Therapeutic Agents Used Cancer TITLE OF INVERTION: Sets

FILE REFERENCE: 689290-76

CURRENT APPLICATION NUMBER: US/60/233,617

FRIOR FLILING DATE: 2000-09-26

FRIOR PLICATION NUMBER: US/60/234,923

FRIOR FLILING DATE: 2000-09-25

FRIOR PLICATION NUMBER: US/60/235,134

FRIOR FLILING DATE: 2000-09-26

FRIOR FLILING DATE: 2000-09-26

FRIOR FLILING DATE: 2000-09-26

FRIOR FLILING DATE: 2000-09-26

FRIOR FLILING DATE: 2000-09-27

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Sequence 10110, Application US/09867701
Fatent No. US20020132237a1
GENERAL INFORMATION:
APPLICANT: Adlate, Paul A.
APPLICANT: Adlate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: UNDBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastERE for Windows Version 4.0
LENGTH: 337
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52;
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; LOCATION: (1)...(337)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10110
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ORGANISM: Homo sapien
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; ORGANISM: Homo sapiens
US-09-954-456-892
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AA206559 2451602.r
AA46382 AJ446382
AL490520 T. brucei
AL700490 DRF2668B
AJ397416 AJ397416
BE265171 601192926
BE7674237 602136968
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             AL452614 T. brucel BI706542 (40703.) AW139708 UI-H-BI1-AW504644 UI-HF-BIN-BF514910 UI-H-BW1-BG961625 PW0-CT064 BI136273 F065587X BQ339760 QV2-NN004 AW6409842 946114F09 BF92697 CM2-NT019 AL629376 fC05901. Y BH635764 100800640 AL484062 T. brucel R44819 yg92a01.1 BH620101 1007064E0 R87939 yo47c09.r1
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B1858096 603385158
AJ450146 AJ450146
BB612952 BB612952
AJ447930 AJ447930
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BI922476 HVSMEm000
BI758440 603022555
AU119633 AU119633
AJ456352 AJ456352
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AL708655 DKF2686J
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                                                                                  December 11, 2002, 16:56:23; Search time 1655.5 Seconds (without alignments) 146.743 Million cell updates/sec
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BH876695 hr32g07.b BB840417 BB840417 R50904 yq70f04.r1 A1384036 dcd5c03.x BQ787218 i151q12.y BQ787218 i151q12.y BA1922046 wn51e08.x BF365993 PM2-NT007 BH78625 fzmb014f0 AA102916 mo16b07.r AW463201 BP20012A AW764260 ur73c09.x BEB10059 218860 MA AQ426561 CITBI-E1- AU155693 AU155693 BB831127 BB831127 BB831127 BB831127 BB831127 BB831127 BA375006 BJ275006 AA811195 vq32c08.r BF34432 602017391 T90046 yel3e05.s1 BB861945 BB861945 AA212895 OOG AQ2 r N AA2126403 AA230931 us37b02.s BH32012 6 C4Q2.r AL260989 AL650989 AW230991 us33b03.y BB303796 601084365 BG231740 naf38f01.	BH098427 RPCI-24-3 BH873765 hp46f08.b A1660101 we55f02.x BG002754 ov4-Gn025	BE810065 218866 MA BM102770 fu32a03.y BH837196 IMCR05001	A1073428 ov46d07.x A1798652 w93se01.x AW296239 UT-H-B12- BB836778 BB836778	BF291788 WHE2204_A C22356 C22356 Rice BH785148 fzmb013f0 AI424915 tg38d07.x AV66847 AV668547 W23819 zb79d06.rl
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## ALIGNMENTS

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RECI-23-442E20.TV RPCI-23 Mus musculus genomic clone RPCI-23-442E20 AZ284882
                                                                                                                                                                                                                                                                             Jao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C. M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-442E20.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 181)
                                                                                                                                AZ284882.1 GI:9526668
                                                                                                                                                                                              Mus musculus
                                                                                                                                                                            house mouse.
                                                                                                                                                       GSS.
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RESULT 1
AZ284882
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ESM Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 226)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sano, R., Shibata, Y., Saito, H., Sano, M., Tominaga, N., Tsunoda, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Yoshido, M., Muramatsu, M. and Hayashizaki, Y. Yoshido Hayashizaki

KIKEN Mouse ESTS (Konno, H., et al. 1999)

Contact: Yoshihide Hayashizaki
Taharatoru, for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI: Female C57BL/6J mouse kidney and/or
Broat genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DHOB electrocompetent cells (BRL Life Technologies).

54 c 25 g 47 t
Tel: 301 838 0200
Eax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/60"
/db_xref="taxon:10090"
/clone="xpr1-23-442E20"
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/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 297)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, Kaikuchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Izawa, M., Kawai, J., Kaikuchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Izawa, M., Swato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Taman, T., Yokota, T., Toninaga, N., Mutanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV067076 29-JUN-1999 AV067076 Mus musculus small intestine C57BL/6J adult Mus musculus cDNA clone 2010200P09, mRNA sequence.
AV067076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length CDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
     Heubner, D., Mewes, H.W., Weil, B. and Wiemann, S.)
                                                                                             Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de;
sequenced by AGGWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp686J0853) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@tzpd.de.
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone=lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15; DB 9; Pred. No. 5.5e+02; Mismatches 0;
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100.0%;
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                                                    Contact: Wambutt R
MIPS
     EST (Wambutt,R., He
Unpublished (1999)
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                  Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999).

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RIKEN full-length enriched, adult male medulla oblongata"
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DKFZp686J0853_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686J0853 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was GAGAGAGAGGATCCAAGAGCTTTTTTTTTTTTTVN 3'), cDNA was
Email: genome-res@gsc.riken.go.jp,
WEL:http://genome-gsc.riken.go.jp,
Saski,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 246)
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Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="medulla oblongata"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 15; DB 10; 100.0%; Pred. No. 5.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Gaps

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EUKaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 393)

8 Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C.
Rapid CDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library

Nat. Genet. 4, 373-380 (1993)

E 94004965

Contact: Adams, MD

The Institute for Genomic Research
93 2 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699453
Fax: 3018699453
Email: mdadams@tigr.org
Seq primer: M13 Reverse.
        /dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old:
isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
a 111 c 99 g 9 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ายชชย9
BST06781 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBL71
5' end similar to p87 transporter-like protein, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo saplens"
/db_xref="ATCC (inhost):85383"
/db_xref="taxon:9606"
/clone="HIBBLI"
/clone="HIBBLI"
/clone="Vector: Lafmid; The IB library was constructed by directional cloning and oligo(dT)-priming in the Lafmid vector, utilizing a three month old infant human brain (total brain):
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                                                                                                                                                                                                                                                                                       /tissue_type="small intestine"
/dev_stage="adult"
/dev_stage="adult"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; ist strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSCIZB021 normalized infant brain cDNA Homo sapiens cDNA clone C-1zb02, mRNA sequence. F07213 G1:672862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2010200P09"
/clone_lib="Mus musculus small intestine C57BL/6J adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 378)

Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Sebastiani-Kabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome and its expression

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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Seq primer: (-21)M13_universal.
    Location/Qualifiers
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1, rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
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/organism="Homo sapiens"
/organism="Homo sapiens"
/olove="c-1zb02"
/clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 15; DB 9; 100.0%; Pred. No. 5.5e+02; ive 0; Mismatches 0;
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/tissue_type="total brain"
                                                        /organism="Mus musculus"
                  Location/Qualifiers
1. .297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genexpress@genethon.fr
Single read.
                                                                                                                                                                                                                                                                                                                                                                                                                                 79 g
                                                                                                                                                          /sex="male"
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Best Local Similarity 100.
Matches 15; Conservative
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Fax: 33160778698
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further
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Hali,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

Location/Qualifiers

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                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 399)
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                                                                                                                                                                                                                                                                                Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Gallus gallus bursal lymphocyte EST
Unpublished (2002)
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="22g1lr1"
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Heinrich-Pette-Institute
                   AJ449549.1 GI:20216770
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                                                                                                                                                                                                                                 Contact: Buerstedde JM
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Matches 15; Conserv
AJ449549
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B1706542 403 bp mRNA linear EST 13-FEB-2002 fg07c03.yl Zebrafish adult retina cDNA Danio rerio cDNA clone 4790765 5' similar to TR:Q9UH03 Q9UH03 BK250D10.3 ;, mRNA sequence.
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S.L., Hillier, L., Rucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
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Washu Zebraitsh EST Project 1998
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Glibrary constructed by: Chandra Tucker and Gregory Niemi DNA
Library constructed by: Chandra Tucker and Gregory Niemi DNA
All Contact Clone
distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germany
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
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/ksex="mixed"
/dev_stage="L-2 years"
/lab_host="E.Coli XL1-Blue MRF' (XL1-Blue MRF')"
/note="Vector: Lambda ZAP II (pBluescript SK-); Site_1:
ECORI; Site_2: Sall; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number: 760"
                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 5.6e+02;
; Mismatches 0;
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100.0%; Pred. No. 5.6e+02;
Live 0; Mismatches 0;
/organism="Trypanosoma brucei"
/strain="TREU927"
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High quality sequence stop: 396.
Location/Qualifiers
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Seq primer: T3 ET from Amersham
                                                      /db_xref="taxon:5691"
/clone="8e07"
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/db_xref="taxon:7955"
/clone="4790765"
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Matches 15; Conservative
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Gaps

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human.

SOURCE ORGANISM

AUTHORS TITLE

JOURNAL

REFERENCE

DEFINITION RESULT 10 AW139708/c

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ACCESSION VERSION KEYWORDS

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UI-HF-BNO-alk-h-12-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079943 5', mRNA sequence.
AW504644
AW504644.1 GI:7142311
EST
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UI-H-BMI-anp-a-11-0-UI.S1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
BF514910
                                                                                                                                                                                                                                                                                                                                                          Eukaryotan Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 400)
NIH-MGC http://mqc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
ECO RI site shown at the beginning of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: M.G. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbryimage/image.html
Seq primer: MI3 Forward
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ilarity 100.0%; Pred. No. 5.6e+02;
Conservative 0; Mismatches 0;
                                                             Score 15; DB 10;
Pred. No. 5.6e+02;
0; Mismatches 0;
                   82
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                 91
   TAG_SEQ=AATGC"
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                                                             Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-remail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
1s likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A.G.E. Consortium/Linu at:
Www.bio.linl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 151-216, >(GGGA
                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 410)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAIIonal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
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/db_xref="taxon:9606"
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TAG_TISSUE=kidney
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                                                                                                                                         AW139708.1 GI:6144426
114 CCTTCTCCCCTGTT 100
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BG961625.1 GI:14379796
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Matches 15; Conservative
         130 CCTTCTCCCCTGTT 116
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BI136273
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The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I.M.A.G.E. Consortium/LLNL at:
www.blo.llnl.gov/bbrp/image/image.html
Seq primer: Ml3 Forward
POLYA-Yes.
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/db_xref="taxon:9606"
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      BF514910.1 GI:11600078
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Matches 15; Conservative
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                                                                                                 Homo sapiens
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| 1. .430 | / organism="Homo sapiens" | / organism="Homo sapiens" | / organism="Homo sapiens" | / organism="Homo sapiens" | / organism="Example | / organism="Site_1" | / organism="Colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-libary was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 / 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                              Bukaryotz, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini; Hominidae, Homo.

1 (bases 1 to 430)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
BG961625 410401-007-C09 CT0642 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Final sampsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-CTO642-240401-007-C09&t3=2001-04-24&t4=1)
Seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \operatorname{Simpson}, A.J. Shotgun sequencing of the human transcriptome with ORF expressed Shotgun
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100.0%; Pred. No. 5.6e+02;
tive 0; Mismatches 0;
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B1136273.1 G1:18017201
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High quality sequence stop: 376.
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Search completed: December 11, 2002, 19:01:29 Job time: 1715.5 secs
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Dias Neto, E. (Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costar, F. F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-
211100-494-c07&t3=2000-11-21&t4=1)
Seq primer: puc 18 forward
Populus balsamifera subsp. trichocarpa.
Populus balsamifera subsp. trichocarpa
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 430)
                                                                                                                                                               Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H., Hiltonen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahlerao, R., Jansson, S. Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, G. and Lundeberg, J.

Content in Populus
Contact: Erlandsson R
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
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/clone_lib="Populus flower cDNA library"
/note="Organ: flower"
                                                                                                                                                                                                                                                                                                                              Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Tel: 46 B 790 8287
Fax: 46 B 245452
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100.0%; Pred. No. 5.6e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rikerl@biochem.kth.se
Location/Qualifiers
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High quality sequence start: 12
High quality sequence stop: 29.
Location/Qualifiers
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Best Local Similarity
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	December 11, 2002, 12:26:07; Search time 1657 Seconds (without alignments) 263.453 Million cell updates/sec
Title: Derfect ecore.	US-09-750-609-10
Sequence:	1 cettetececetgit 15
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 seqs, 14551402878 residues
Total number of	Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries GenEmbl:* Database :

em_ro:*
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em_htgo_mus:* em_htgo_other:* em_htg_vrt:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description	00	-	AF232676 Sus scrof	L01121 Gallus gall	AF312211 Homo sapi	ABUI82/9 HOMO Sapi AL035357 Fuqu rubr	7		AC107069 Homo		AL283832 AC131033	AC097798		AC129736	AL158205 Humar		ACUZIY6/ HOMO AC111526 Ratti	ACILITIES SECTION ACILIARY RALTUS	ACIU5876 Rattus		Continuation (2	AC018785 Homo s	AC120946 Rattus	ACII/134 AL449363	AC121163 Rattus	AC11881	Z93942 Human DNA	D50453 Bacillus s	AC124033 Kartus AC094249 Rattus	AC113827 Rattus		ACII+050 Nattus II	NTS	bna linear PRI 04-APR-2001 e for alpha3 type IV collagen, exon	44	gene.	Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	.er,L., Cohen-Solal,L., Mollet,G., br,M.C. and Antignac,C.
SUMMARIE	ID	HSA288489 AF506010	AK021867	AF232676	CHKTGFBA	AF312211	FR092H06	AE009810	AF14461/ BSSRFAP	AC107069	AL138734	AC131033	AC097798	AC120156 AL391356	AC129736	AL158205	HSJ132F21	AC021967	AC116184	AC105876 AC103237 2	AC125066_2	AC125102_1 AL591493	AC018785	AC120946	AC11/154 AL449363	AC121163	AC12813	HS230119	D50453	AC124033 AC094249	AC113827	AC112466	AC114830	ALIGNMENTS	190 bp COL4A3 gene	1	:13559182 collagen; col4a3	Chordata;	., Forest 1,C., Gubl
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	Score	15	15	15	12	15	12	15	15	15	15	15	15	15	15	15	15	. T	15	15	15	15	15	15	15	15	15	15	15	15	15	15	CT					-	
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Sksdiookddssivpwllsfkrgtaleeggnkiviketgyffiygovlytdyffamgh
Liorkkahvegddlslvylfrcionmposypunscytagiakleegdeloliiprrra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the TNF family
Structure of the human type IV collagen gene COL4A3 and mutations in autosomal Alport syndrome J. Am. Soc. Nephrol. 12 (1), 97-106 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Schneider K., Kolthow, S., Schneider, P., Goebel, T., Kaspers, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                         Direct Submission
Submitted (28-MAR-2000) Antignac C., U423, INSERM, Hopital
Necker-Enfants malades 149 rue de Sevres, 75015 Paris, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus TNF family B cell activation factor (BAFF) mkNA, AF506010.1 GI:22087370
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Schneider,K., Kolthow,S., Schneider,P., Goebel,T., Kaspers,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission Submitted (24-APR-2002) Virology, University of Freiburg,
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/protein_id="AAM90951.1"
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                                                                                                                                                                                                                                                                                                                                                                                                Length 190;
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Location/Qualifiers
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/usedin=AJ288487:cal_CDS
                                                                                                                                                                            1. .190
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/db_xref="taxon:9031"
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                                                                                                                                                                                                                              51. .140
/gene="COL4A3"
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                                                                               2 (bases 1 to 190)
Antignac, C.
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Best Local Similarity 100.
Matches 15; Conservative
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AF506010/c
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RLGVHT&GADIDALCVAPRHVERSDPROSFREKKINDGSROURDEILHLypnker
RLGVHT&RADILARAKLMARREGIYSNMLGEFGGGVSAMLVARTCQLYPNAAASTLUHKPPROFF
RELTRAVKLWARREGIYSNMLGEFGGVSAMLVARTCQLYPNAAASTLUHKPPROFF
KWEWPNPVLLKOPEENGLYBVWDPRVPSDRYHLMPITTPAARONSTYRYTSTRY
VWPEBRRGGIAVTDEILQFGKSDWSKLLEPPNFRORKHYTVLTAAASTEBHLEWYGL
VESKIRVLVGNLERNEFITTAHVNPQSFPONKEHHKDNNYVSMWFLGIIFRRVBNAES
VNIDLTYDIOSFTDTVYROANNINMKEGMKIEATHVKKRQLHHYLDAEIL"
                                                                                                                                                                                                                                                                                                                                                             AK021867

Homo sapiens cDNA FLJ11805 fis, clone HEMBA1006278, moderately similar to POLY(A) POLYMERASE (EC 2.7.7.19).
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Direct Submitssion

Bubmitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomicselri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library

Construction, 5'-$ 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center

etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai,T., Ota,T., Hayashi,K., Suqiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomira,Y., Togiya,S., Komai,P., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                             AK021867
AK021867.1 GI:10433146
Oligo capping; fis (full insert sequence).
Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to
MRNA, clone_lib:HEWBA1 clone:HEWBA1006278.
                                                                                                                                                      Gaps
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0
                                                                                                 Length 600;
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                                                                                         100.0%; Score 15; DB 5; I
100.0%; Pred. No. 1.2e+03;
iive 0; Mismatches 0;
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Location/Qualifiers
1. 1689
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
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KISLDGDGTFFGAVRLL"
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                                                                                                                                                                                                                   75 CCTTCTCCCCCTGTT
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 7 Row: 1 Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTGTWYORWGVRALSLGGOVWGNFLSCFGPEYRRITLMMMGVWFTMSFSYGLTVWFP
DMIRHLQAVDYASARTVEFGERVEHYPENTLENDLHRGGOVFROKETGLARKSYSFE
DDSLFREGYFBDYTSSNTFRNGTFINTVFTVATDLFFXKFVNSKLINSTFLHNKEGCPL
DVTGTGEGAYMVYFVSFLGTLAVLPGNIVSALLMDKIGRLRMLAGSSVMSCVSCFFLS
FGNSESAMIALLCLEGGVSTASWNALDVLTVELYPSDKRTTAFGFLNALCKLAAVLGI
STESPGGITKAAPILFASAALALGSSLALKLPETRGOVLO"

8 850 C 868 9 810 t
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L01121
L01121 GI:511842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPESPRFFLENGKHDEAWMVLKQVHDTNMRAKGHPERVFSVTHIKTIHQEDELIEIQS
                                                                                                                                                                                                                                                                                                                                                                                  contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3190)
                                                                                                                      Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 15; DB 9; Length 3190; 100.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 3190
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/clone="IMAGE:3509807"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Rubin Laboratory
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Matches 15; Conservative
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CHKTGFBA/C
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                                                                                                                                                                                                                    AF232676 1721 bp mRNA linear MAM 22-NOV-2000 Sus scrofa prophet of pit-1 (Prop-1) mRNA, complete cds. AF232676.1 GI:11275672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-FEB-2000) Biology, Indiana University Purdue
University Indianapolis, 723 West Michigan Street, Indianapolis, IN
46202-5132, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"prophet of pit-1"

/protein_id="AAG3702.1"

/db_xref="G1:11275673"

/translation="MEAEGRREGGKPRKGRVCSSLWPEGYPAAGTLTARVDISTRPYR

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PPPMTCFPHPYNHALPSQPSTGGSFARHPQSEDWYPTLHPTPTGHLPCPPAPPVLPLS
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1721)
Sloop, K.W., McCutchan Schiller, A., Smith, T.P., Blanton, J.R. Jr.,
Rohrer, G.A., Meier, B.C. and Rhodes, S.J.
Blochemical and genetic characterization of the porcine Prophet of
Pit-1 pituitary transcription factor
Mol. Cell. Endocrinol. 168 (1-2), 77-87 (2000)
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                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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McCutchan Schiller, A.L., Sloop, K.W., Blanton, J.R. Jr., Meier, B.C.
                                           Gaps
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IMAGE:3509807, mRNA, partial cds.
BC000776
100.0%; Score 15; DB 9; Length 1689; 100.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1721;
                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                       Indels
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100.0%; Pred. No. 1.1e+03;
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/note="transcription factor"
                                         Mismatches
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/db_xref="taxon:9823"
1. .1721
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Conservative
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                                       Conservative
                                                                                                   123 CCTTCTCCCCTGTT 109
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                                                                             1 CCTTCTCCCCCTGTT 15
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                    Similarity
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Gaps

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Indels

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Cell. Biol. 21 (16), 5614-5623 (2001)
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/organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                (bases 1 to 3752)
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Matches 15; Conserv
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AUTHORS
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MEDLINE
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VERSION
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/db_xxef="G1:511843"

/db_xxef="G1:511843"

/db_xxef="G1:511843"

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LLNSPLPLVWKLKTERLAPGIRKVFYSGSIVWFEKONFSLSAFTERNFPRENEHL
LQWARKERGAYFSFTELKISRNIYIRVGEDOVFPPTCNIEKNFLSARIERNVTLKKCK
KSVNNVIKSHDVQKREAVITENIYIRVGEDOVFPPTCNIEKNFLSLNXLAGYLQPRRA
EGCLMSNLVOBREVHITELITPNSNPYSAFQVDITUDIFSQGARLERNVTLIKKCK
KSVNNVIKSHDVQKALEVTTSNSIGFCKETERSMTMSKSVIPDIPSGHESLIKWAYEH
KYSPVTSYTRAPVANRFHLQLEHTEENNDEEDHSLPPELTELLHGAKNPALSDGLTFP
FHINRGGHETGGGIPPSRDSVDTLINNBFEBLSLSKREPEBVGGARDVALSIKCDBK
VMTVAVEKDSLQASGYTRTELSLIDHSCKARNNGTHFILESPRNCGTRTSYILDKIV
YFNSIVIQLSSPAEGSSFDDDDMESGDNGFPGDADEGDVTFSNNPEIAFNCTLHQPER
DFINRAMFWPPERPHITNVTFNNRLYTENHALTENFRENGSTRENGVRADIG
                                                                                                                                                                 1 (bases 1 to 3347)
Barnett,J.V., Moustakas,A., Lin,W., Wang,X.F., Lin,H.Y.,
Barnett,J.V. and Mass,R.L.
Cloning and developmental expression of the chick type II and type
III TGF beta receptors
Dev. Dyn. 199 (1), 12-27 (1994)
8167376
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FVFKPIFNISLLFLHCELTLCTNIDKDTQRLPKCVPPDEACTSLNVDMILAMHINKKT
FTKPLVITHEGKPEDSSLPKSNVRQPSVFYGLDTLTVVGIAFAAFVIGALLTGALWFI
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Homo sapiens neo-poly(A) polymerase mRNA, complete cds.
AF312211
                                                        Gallus gallus (library: lambda zap) embryonic brain cDNA to mRNA. Gallus gallus gallus Gallus Gallus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
TGF-beta; betaglycan; plasma membrane; transforming growth factor-beta receptor; transforming growth factor-beta type III
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Topalian, S.L., Kaneko, S., Gonzales, M.I., Bond, G.L., Ward, Y. and
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/product="transforming growth factor-beta type III
receptor"
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712 c 708 g 931 t
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                                                                                                                                                                                                                                                                                                                                                                               /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_lib="lambda zap"
152. .2677
                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="brain"
/dev_stage="embryonic"
/germline
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/translation="WKEMSANTVLDSQRQQKHYGITSPISLASPKEIDHIYTQKLIDA
/translation="WKEMSANTVLDSQRQQKHYGITSPISLASPKEIDHIYTQKLIDA
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VESKIRVLGGNLERREFITLAHVNPQSFPGRKEHHKDNNY SWWFLGIIFRRVENAES
VNIDLYDIGSFTDTVYRQANNI NMLKEGMKIERATHVKKQLHHYLPRAEILQKKKKQS
LSDVNRSSGGLQSRRLSLDSSCLDSSRDTDMGTPRNSPASKSDSPSVGETERNSAEPA
AVIYERPLESPRAGGLSIPVIGAKVUSTYKTVGPPRAAESPRA
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KSVDAGLGESMPTTTDTSRKKRLDSSELDGTFKRLDVEKFIRLESTRENBERRR
RSVDAGGGSSMPTTTDTSRKKRLDSSELPROSSSPVPANNIRVIKNSIRLITHNR
Topalian, S.L., Gonzales, M.I., Wang, X. and Wang, R.-F.
Direct Submission
Submitted (09-OCT-2000) Surgery Branch, NCI, National Institutes of
Health, Building 10, Room 2B47, Bethesda, MD 20892, USA
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Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
Tanaka,A., Kotani,H., Nomura, N. and Ohara,O.
The Could sequences of unidentified human genes. XI.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro
90087487 (5), 277-286 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to Homo sapiens poly(A) polymerase protein
(PAP) encoded by GenBank Accession Number X76770"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-OCT-1998) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
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Catarrhini; Hominidae; Homo.
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Ohara,O., Suyama,M., Nagase,T., Ishikawa,K. and Kikuno,R.
Direct Submission
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Homo sapiens mRNA for KIAA0736 protein, complete cds.
AB018279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="neo-poly(A) polymerase"
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ilarity 100.0%; Pred. No. 1.1e+03;
Conservative 0; Mismatches 0;
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4930. .5051,5125. .5247,5324. .5511,6159. .6303,6400. .6543
6663. .6848 7063. .7131,7228. .7342,7460. .7587,7693. .7787
7973. .8122,9912. .>9014)

join(1812. .1844,2092. .2116,3187. .3283,3527. .3653,
4037. .4092,4204. .4308,4394. .4487,4572. .4654,4730. .4845,4730. .5051,5125. .5247,5324. .5511,6159. .6303,6400. .6543,7973. .8122,8912. .9014)
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WRFLEHKGPYEAPPYEPLDDKVKFYYDGKLMKLAAPAEEVATFFAKMLDHEYTTKDVF
KRFFKDWRKEMTSEEKSKTTDLNKCNFAGMNPYFKAQESAKOMSKEEKQKIKEDNE
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KHPRPPPGTKWKEVRHDNKVTWLASWTENIQGSIKYIMLNPSSRIKGEKDWQKYETAR
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FDRAMTSILAKHLQELMDGLTAKVFRTYNASITLQQQLKELSGSDDSYPAKILSYNRA
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KRAVEVKRKAVQRIPEGLMK.QVQATDREENKQIAGTSKLNYLDPRISVAWCKFGI
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PKKEKENGYVRDLSPAAIKNEPEEDNGLYSSPQHNKTSRRECDDEEFDCKPKKVKTEH
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/gene="toplalpha"
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/gene="toplalpha"
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/gene="toplalpha"
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3187. .3283
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join(<1812. .1844,2092. .2116,3187. .3283,3527. .3653,
4037. .4092,4204. .4308,4394. .4487,4572. .4654,4730. .4845,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MEEGFRDRAAFIRGAKDIAKEVKKHAAKKVVKGLDRVQDEYSRR
SYSRFEEEDDDDDFPAFSDGYYRGEGTQDEEEGGASSDATEGHDEDDEIYEGEYQGIP
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Fugu rubripes cosmid 092H06 genomic DNA fragment, toplalpha gene.
AL035357
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1 (bases 1 to 11001)
Smith, S. F., Metcalfe, J. and Elgar, G.
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Submitted (01-FEB-1999) Smith S.F., Fugu Group, UK HGMP Resource
Centre, Wellcome Genome Campus, Hinxton Hall, Hinxton,
Cambridgeshire, CB10 1SB, UNITED KINGDOM
Location/Qualifiers
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                                                                                                                                   /tissue_type="brain"
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/dev_stage="adult"
1. .4353
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1812. .9014
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/db_xref="taxon:9606"
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toplalpha gene; topolsomerase I.
Takifugu rubripes.
Takifugu rubripes
                                                                                                                                                                                                                                                                                         435. .2663
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Best Local Similarity 100.
Matches 15; Conservative
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FR092H06/c
LOCUS
DEFINITION
ACCESSION
   source
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JOURNAL
REFERENCE
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KEYWORDS
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7mmber 18

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Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
1 (bases 1 to 11896)
Fitz-Gibbon,S.T., Ladner,H., Kim,U.J., Stetter,K.O., Simon,M.I. and
Miller,J.H.
                                                                                                                                                                                                                                                                                                                                                                       AE009810 11896 bp DNA linear BCT 16-JAN-2002 Pyrobaculum aerophilum strain IM2 section 65 of 201 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum
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Fitz-Gibbon S.T., Ladner, H., Kim, U.-J., Stetter, K.O., Simon, M.I. and Miller, J.H.
Direct Submission
Direct Submission
Submitted (12-DEC-2001) Microbiology and Molecular Genetics, University of California, Los Angeles, 405 Hilgard Ave, Los Angeles, CA 90095-1489, USA
Angeles, CA 90095-1489, USA
I. 11896
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                                                                                                                                                                                              Gaps
                                                                                                                                                                                              ;
                                                                                                                                                      Length 11001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99 (2), 984-989 (2002)
11792869
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Pred. No. 9.8e+02;
; Mismatches 0;
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AE009810 AE009441
AE009810.1 GI:18159943
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illarity 100.0%;
Conservative 0
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Best Local Similarity
Matches 15; Conserv
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AE009810/c
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REFERENCE
AUTHORS
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/note="DNA metabolism; DNA replication, recombination, and
                                                                                                                                                                                                                                                                                                                                        LNDFRGKYPRYNYPGVLVSP<sup>N</sup>NSQEGLEWILTLPGDLYIAMEQIYLDSGMVPLILQHQ
RYYAVVARTNADINVAVDDDIVAKIIVVGDYVYVGSINLGYYSIQRNREVGLLIHNPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPLLRKVKLCVVADFPFGALPTASRIALVSRLAEVADEIDVVAPIGLVKSRRWAEVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLISVVGAAGGRVVKVITEEPYLRDEERYTLYDIIAEAGAHFIKSSTGFAEEAYAARQ
GNPVHSTPERAAAIARYIKEKGYRLGVKMAGGIRTREQAKAIVDAIGWGEDPARVRLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="WFIDIEAPAPLKAVVKRCRFKEEYNVELFLEGERLCHVKIFTGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Fatty acid and phospholipid metabolism; Other"
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TFIRCIAGLETPTKGRILEGDAPVIDVERGINIPPAKRNVGMVPGNWALTPHMKVFDN
IAFPLKIKKLPKSEIERRYKEVABALEISINLLDRYPRQLSGGOORVALARALVKEPO
VOLLMDEPPENLISAREFYSLGRRIKITTILVTHDQHDAYALADRLMVINGV
VQOISTTDEVLNNPANISAREFYSLGRRIKITTILVTHDQHDAYALADRLMVINGV
VQOISTTDEVLNNPANIFVAQFRGDPINILEGEGRGBHYDLGBLKIPIPAPQGKLQV
GIRPTDIYIADQPLSPEDLELKPGRVLLVEYLGFTPVAVVKWERIEVRAVMYNKLKEG
SLARVFLKKEGVKLFQNGVRIK"
                       VKTLPDFSQENRVAAGNILPRIRMTVLYYYANKYNLLVMGTGDRSELLLGYFTRYGDG
GVDFLPIGSLFKLQVRELAARLGFADIAKKPSSPRLWQGHTAEGELGASYEVIDQVLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILGYSWHMVEPWRFTEAPVYAIQKLLKKLGTEIDSFDYFEANEAFAVVNVLVHRILGV
PYEKLNVFGGAIALGHPLGASGARIVTTLISVLRNKGGRRGIAALCHGTGGGTAIALE
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TSKEAYETGFGIDFGAYAVLAVPELEQYVLKGLERHYADAKRATEIVSSQRYKLITTG
EIAAVAVEENVPPAPLMNALIDEKALNGPVLIVVKDRRNPGAYTVWRPDRYANIIDFR
STVAAALAVEALGRQRVLGLLMPSLYTPPEDLKDALDVINALGVEWKRVDJTPIYDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEEAEMVAREHKMTREELDWVAYESHMRAWRATENKWFDDLEPIEGELGGVYVKLERD
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                                                                                                                                                                                                                        'note="Fatty acid and phospholipid metabolism;
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complement(2652..3722)
/gene="PAE1222"
                                                                                                            complement(1424. .2608)
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Avalos-Ramirez,R., Orlich,M., Thiel,H.-J. and Becher,P.
Complete genomic sequences of pestiviruses from giraffe and
reindeer: evidence for the presence of two novel species within the
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Lelphorgtrdiptrlkdlprkgdcrsgnnkgpvsgvyikpgpvyyodysgpvyhrap
                                                                                                                                                                                                                                                                                                                                           pestivirus giraffe-1 H138.
pestivirus giraffe-1 H138
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                                                                         VRL 23-AUG-2001
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                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 12602)
Becher, P., Orlich, M., Kosmidou, A., Konig, M., Baroth, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Avalos-Ramirez, R., O'lich, M., Thiel, H.J. and Becher, P. Evidence for the presence of two novel pestivirus species Virology 286 (2), 456-465 (2001)
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    Length 11896;
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                                                                                                                                                                                                                                       AF144617 12602 bp RNA
Pestivirus giraffe-1 H138 complete genome.
  Score 15; DB 1;
Pred. No. 9.7e+02;
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                                              Mismatches
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tive 0;
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Becher, P. and Orlich, M.
Direct Submission
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AF144617.2 GI:15282441
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    Query Match
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CRYPTHIPFGSRMPGTSDQREECGFLQYRARGQLFLRNLPILATRWKFLAWGNGLGSEV

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REFERENCE AUTHORS

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NOLREFKSSLYKLFTVSLEYQVWQWQKEEDLAFLTEPIFSGSGLNDVSIHVKDRWDTG
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ELASGSERFKEDISHFIDHVLSEQEYAQSRREFRKDAFWNKOFESVPELVSLKRNASA
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GRTAAVLCERSMDMIVSILAVLKSGSAYVPIDPEHPIQRMQHFFRDSGAKVLLTQRKL
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ANILRTVKETNYLSITEQDTILGLSNYVFDAFMFDMFGSLLNGAKLVLIPKETVLDMA
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2 (bases 1 to 32802)
Cosmina, P., Rodriguez, F., de Ferra, F., Grandi, G., Perego, M.
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                                                                                                                                                                          B.subtilis srfA-sfp gene region for surfactin synthetase. X70356 X70357 X70358 X70356 L GI:396480 surfactin synthetase. Bacillus subtit
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/strain="W168 derivative of JH642"
/db_xref="taxon:1423"
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/db_xref="GI:396481"
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Bacillus subtilis
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DTSSNPLFDAVFSMQNANIKDLTMKGIQLEPHPFERKTAKFDLTLTADETDGGLTFVL EYNTALFKQETIERWKQYWMELLDAVTGNPNQPLSSLSLYTETEKQALLEAWKGKALP VPTDKTVHQLFEETAQRHKDRPAVTYNGQSWTYGELNAKANRLARILMDGGISPDDRV SYTGDVILLDGSRTILSLPLDENDEENPETAVTAENLAYMIYTSGTTGQPKGVMV EHHALVNLCFWHHDAFSMTAEDRSAKYAGFGFDASIWEMFPTWSIGAELHVIEEAIRL DIVRLNDYFETNGVTITFLPTQLAEQFMELENTSLRVLLTGGDKLKRAVKKPYTLVNN YGPTENTVVATSAEIHPEEGSLSIGRAIANTRVYILGEGNQVQPEGVAGELCVAGRGL ARGYLNREDETAKRFVADPFVPGERMYRTGDLVKWTGGGIEYIGKIDQQVKVRGYRIE LSEIEVQLAQLSEVQDAAVTAVKDKGGNTAIAAVYTPESADIEALKSALKETLPDYMI PAFWVTLNELPVTANGKVDRKALNEPDIEAGSGEYKAPTTDMEELLAGIWQDVLGMSE VGVTDNFFSLGGDS1KG1QMASRLNQHGWKLEMKDLNQHPT1EELTQYVERAEGKQAD QGPVEGEVILTP1QRWFFEKNFTNKHHWNQSVMLHAKKGFDPERVEKTLQAL1EHHDA LRMVYREGGEDVIQYNRGLEAASAQLEVIQIEGGAADYEDRIEREAERLGSSIDLQEG GLLKAGLFQAEDGDHLLLAIHHLVVDGVSWRILLEDFSAVYTQLEQGNEPVLPQKTHS HQVKIRGQAIELGEIEHQLQTHDRVQESVVLAVDQGAGDKLLCAYYVGEGDISSQEMR EHAAKDLPAYMVPAVFIQMDELPLTGNGKIDRRALPIPDANVSRGVSYVAPRNGTEQK LAQVIASAEKGTAASISPAEKQDTYPVSSPQKRMYVLQQLEDAQTSYNMPAVLRLTGE LDVERLNSVMQQLMQRHEALRTTFEIKDGETVQRIWEEAECEIAYFEAPEEETRIVS EFIKPPKIDQLPLFRIGLIKHSDTEQVLLFDMHHIISDGASVGVLIEELSKLYDGETL EPLRIQYKDYAVWQHRFIQSELYKKQEEHWLKELDGELPVLTLPTDYSRPAVQTFEGD RIAFSLEAGKADALRRLAKETDSTLYMVLLASYSAFLSKICGQDDIIVGSPVAGRSQA DVSRVIGMFVNTLALRTYPKGEKTFADYLNEVKETALSAFDAQDYPLEDLIGNVQVQR GVLTKPSLEMSAAVLGVLKAGAAFVPIDPDYPDQRIEYILQDSGAKLLLKQEGISVPD FAEYAERLQDFANSKAFLKEKEYWSQLEEQAVAAKLPKDRESGDQRWKHTKTIEFSLT AEETEQLITTKVHEAYHTEMNDILLIAFGLAMKEWTGQDRVSVHLEGHGREEIIEDLTI SRTVGWFTSMYPMVLDMKHADDLGYQLKQMKEDIRHVPNKGVGSGILRYLTAPEHKED VAFSIQPDVSFNYLGQFHQMSHPPFFTTSHLPSPHSLSPETEKPNALDVVGYIENGKL TMSLAYHSLEFHEKTVQTFSDSFKAHLLRIIEHCLSQDGTELTPSDLGDDDLTLDELD /translation="MSKKSIQKVYALTPWQEGMLYHAMLDPHSSSYSTQLELGIHAAF DLEIFEKSVNELIRSYDILRTVFVHQQLQKPRQVVLAERKTKVHYEDISHADENRQKE HIERYKQQVQRQAFNLAKDILFKVAVFRLAADQLYLAWSNHHIMMDGWSMGVLMKSLF QNYEALRAGRTPANGQGKPYSDYIKWLGKQDNEEAESYWSERLAGFEQPSVLPGRLPV YPGKTWTVKIKYNGAAFDSAFIERTÄEHLTRMMEAAVDQPAAFVREYGLVGDEEQRQI VEVFNSTKAELPEGMAVHQVFEEQAKRTPASTAVVYEGTKLTYRELNAAANRLARKLV MIEHKSILRLVKNÄGYVPVTEEDAMAQTGAVSFDAGTFEVFGALLNGAALYPVKKRHV LDAKQFAAFLREQSITTMWLTSPLFNQLAAKDAGMFGTLRHLIIGGDALVPHIVSKVK QASPSLSLWNGYGPTENTTFSTSFLIDREYGGSIPIGKPIGNSTAYIMDEQQCLQPIG APGELCVGGIGVARGYVNLPELTEKQFLEDPFRPGERIYRTGDLARWLPDGNIEFLGR IDNQVKVRGFRIELGEIETKLNMAEHVTEAAVIIRKNKADENEICAYFTADREVAVSE LRKTLSQSLPDYMVPAHLIQMDSLPLTPNGKINKKELPAPQSEAVQPEYAAPKTESEK KLAEIWEGILGVKAGVTDNFFMIGGHSLKAMMMTAKIQEHFHKEVPIKVLFEKPTIQE LALYLEENESKEEQTFEPTRQASYQQHYPVSPAQRRMYILNOLGQANTSYNVPAVLLL EGEVDKDRLENAIQQLINRHEILRTSFDMIDGEVVQTVHKNISFHLEAAKGREEDAEE ADLELPQIHYKDYAVWHKEQTNYQKDEEYWLDVFKGELPILDLPADFERPAERSFAGE RVMFGLDKQITAQIKSLMAETDTTMYMFLLAAFNVLLSKYASQDDIIVGSPTAGRTHP DLQGVPGMFVNTGALRTAPAGDKTFAQFLEEVKTASLQAFEHQSYPLEELIEKLPLTR VADIWAQVLQAEQVGAYDHFFDIGGHSLAGMKMPALVHQELGVELSLKDLFQSPTVEC KKDEYVNKEYSFTWDETLVARIQQTANLHQVTGPNLFQAVLGIVLSKYNFTDDVIFGT VVSGRPSEINGIETMAGLFINTIPVRVKVERDRAFADIFTAVQQHAVEAERYDYVPLY EIQKRSALDGNLLNHLVAFENYPLDQELENGSMEDRLGFSIKVESAFEQTSFDFNLIV EHGLQKGETAAIMNDRSVETVVGMLAVLKAGAAYVPLDPALPGDRLRFMAEDSSVRMV LIGNSYTGQAHQLQVPVLTLDIGFEESEAADNLNLPSAPSDLAYIMYTSGSTGKPKGV IIKAFVQPFELNRAPLVRSKLVQLEEKRHLLLIDMHHIITDGSSTGILIGDLAKIYQG DTSRSPLFSVMFUMQNMEIPSLRLGDLKISSYSMLHHVAKFDLSLEAVEREEDIGLSF EGIIVSLDDGKWRNESKERPSSISGSRNLAYVIYTSGTTGKPKGVQIEHRNLTNYVSW FSEEAGLTKRRADGNDKTVLLSSYAFDLGYTCMFPVLLGGGELHIVQKETYTAPDEIA HYIKEHGITYIKLTPSLFHTIVNTASFAFDANFESLRLIVLGGEKIIPTDVIAFRKMY **DYATALFKDETIRRWSRHFVNIIKAAAANPNVRLSDVDLLSSAETAALLEERHMTQIT** EATFAALFEKQAQQTPDHSAVKAGGNLLTYRELDEQANQLAHHLRAQGAGNEDIVAIV MDRSAEVMVSILGVMKAGAAFLPIDPDTPGERIRYSLEDSGAKFAVVNERNMTAIGQ) /db_xref="SWISS-PROT:004747" /protein_id="CAA49817.1" /db_xref="G1:396482" /transl_table=11 /gene="srfA2" 10780. 21543 /gene="srfA2" /codon_start=1 .21543 KLMEIF" 10780.

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GVTDNFFSLGGDSIKGIQMASRLNOHGWKLENKULEQHPTIEELTQYVERAEGKQADQ
GPVGEVILTPIQRWFFEKNFTNKHHWNGSVMLHAKKGFDPERVEKTLQALIEHDAL
RWYREENGDIVQYYVEYGESEVYDSTETVDLYGSDEEMLRSQIKLLANKLQSSLDLRNG
PLLKAAESYRTEAGDHLLIAVHHLVVDGVSWRILLEDFASGYMQAEKEESLVFPQKTNS
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GPTENTVVATSAEIHPEEGSLSIGRAIANTRVYILGEGNQVQPEGVAGELCVAGRGLA
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SEIEVQLAQLSEVEDRAVTRVKDKGKGNTAIAAYVTPETADIEALKSTLKETLPDYMIP
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PEISFNYLGQFDSEVKTDFFEPSAFDMGRQVSGESEALYALSFSGMIRNGRFVLSCSY
NEKEFERATVEEEMERFKENLLMLIRHCTEKEDKEFTPSDFSAEDLEMDEMGDIFDML
RADDQVKIRGYRIELGEIETVMLSLSGIQEAVVLAVSEGGLQELCAYYTSDQDIEKAE
                                                                                                                                                                                                                                                                          RQLAAYMEASAVSGGHQVLKPADKQDMYPLSSAQKRMYVLNQLDRQTISYNMPSVLLM
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EDTKHLLTDVHQPYGTEINDILLSALGLTWKEWTKGAKIGINLEGHGREDIIPNVNIS
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PFGAVGELCISGMGVSKGYVNRADLTKEKFIENPFKPGETLYRTGDLARWLPDGTIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGRIDDQVKIRGHRIELEEIEKQLQEYPGVKDAVVVADRHESGDASINAYLVNRTQLS
                                                                                                  LRYQLSLTLPSHMIPAFFVQVDAIPLTANGKTDRNALPKPNAAQSGGKALAAPETALE
                                                                                                                                                                                 ESLCRIWQKTLGIEAIGIDDNFFDLGGHSLKGMMLIANIQAELEKSVPLKALFEQPTV
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21580. .25404
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21580. .25404
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gene CDS

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IAGISAYLKNGGSDGLQDVTIMNQDQEQIIFAFPPVLGYGLMYQNLSSRLPSYKLCAF
DFIEEEDRLDRYADLIQKLQPEGPLTLFGYSAGCSLAFEAAKKLEEQGRIVQRIIMVD
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Gaps
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0
100.0%; Score 15; DB 1; Length 32802; 100.0%; Pred. No. 9e+02; 0; Mismatches 0; Indels 0
                                                                           29177 CCTTCTCCCCTGTT 29163
                              Conservative
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Best Local Similarity
Matches 15; Conserv
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RESULT 13 AC107069/c

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PRI 29-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.H.
Direct Submission
Submitted (15-JAN-2002) Genome Sequencing Center, Washington
Submitted (15-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 34578)
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Submitted (13-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 34578)
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                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 34578)
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing Center, Washington 4444 Forest Park Parkway, St.
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AC107069 34578 bp DNA linear PRI 29-M
Homo sapiens BAC clone RP11-249A8 from 2, complete sequence.
AC107069
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                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 34578)
Scott,K., Kozlowicz,A., Spalding,L. and Trani,L.
The sequence of Homo sapiens BAC clone RP11-249A8
Unpublished (2001)
3 (bases 1 to 34578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                    Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (04-APR-2002) Genome
University School of Medicine,
MO 63108, USA
5 (bases I to 34578)
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                                                                                                                              Homo sapiens.
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Louis all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc MAPPING INFORMATION: restriction digest.

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male

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repeat_region
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donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                 NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-495023, 2000 bp overlap;
the clone sequenced to the right is RP11-563C6, 2000 bp overlap.
Actual start of this clone is at base position 126621 of
                                                                                                                                                                                                                                                                                                                                                                             565. .616

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804. .1128

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/rpt_family="MER2_type"

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565, .616
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/rpt_family="AT_rich"
12930. .12965
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10910. .11214
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                                                                                                                                                                                                                  Location/Qualifiers
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Human DNA sequence from clone RP1-310P17 on chromosome 6. Contains GSSs, complete sequence.
AL138734.6 GI:8388469
HTG.
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Matches 15; Conservative C
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/Calegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
RPI-310P17 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: POYPART: This sequence is not the entire insert of clone
RPI-310P17 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RPI-310P17 is at 1 in this sequence. The true left end of clone RPI-310P17 is at 1 in this sequence.
                                                                                                                                                                                                                                During sequence assembly data is compared from overlapping clones. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1924. .2090
/note="LimbB repeat: matches 6005. .6171 of consensus"
2151. .2266
/note="LimbB repeat: matches 5874. .5991 of consensus"
                                                                                                                              Direct Submission
Submitted (21-701-2000) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
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note="LIMB8 repeat: matches 5147. .5429 of consensus"
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'note="LTR17 repeat: matches 1. .780 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(428. .891)
/note="match: GSS: Em:B53078"
complement(580. .878)
/note="match: GSS: Em:AQ269829"
1740. .1867
/note="MIR repeat: matches 20. .146 of consensus"
                              Chordata; Craniata; Vertebrata; Eutele
Primates; Catarrhini; Hominidae; Homo
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/note="AluSq_repeat; matches 1.
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note="match: GSS: Em:AQ508138"
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/note="match: GSS: Em:AQ316392"

    .43347
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="6"
/clone="RP1-310P17"
/clone_lib="RPCI-1"
                                                                            (bases 1 to 43347)
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                                                                                                          Tromans, A.
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ORGANISM
                                                                            REFERENCE
AUTHORS
                                                                                                                                TITLE
JOURNAL
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/ note="AluSqyx repeat: matches 71. .308 of consensus" 1573. .15790
//note="AluSqyx repeat: matches 1. .152 of consensus" 15822. .16105
//note="LiPAl6 repeat: matches 5830. .6110 of consensus" 16106. .16416
//note="LiPAl6 repeat: matches 1. .313 of consensus" 1647. .17711
//note="LiPAl6 repeat: matches 4517. .5830 of consensus" 17737. .18032
//note="LiPAl6 repeat: matches 77. .314 of consensus" 17737. .18032
//note="LiPAl6 repeat: matches 4125. .4510 of consensus" 18427. .18706
//note="LiPAl6 repeat: matches 3826. .4124 of consensus" 18703. .19271
//note="LiPAl6 repeat: matches 5774. .5331 of consensus" 18703. .19271 /note="35 copies 2 mer tt 68% conserved"
21747. .21896
/note="LIMD3 repeat: matches 7476. .7579 of consensus"
complement(21823. .22281) 19949. .20211 /note="L2 repeat: matches 1194. .1452 of consensus" 20944 .2113 /note="AluSg/x repeat: matches 129. .299 of consensus" /note="HERVL repeat: matches 1757. .1969 of consensus" 12998. .13299 .5956 of consensus" note="AluSq/x repeat: matches 1. .133 of consensus" 5732. .7036 /note="AluS repeat: matches 152. .170 of consensus" 15499. .15731 .2750 of consensus" AluY repeat: matches 168. .311 of consensus" .11158 'note="L2 repeat: matches 2290. .2750 of consensus" .2147 of consensus" 'note="AluSp repeat: matches 1. .305 of consensus" .282 of consensus" 0265. 8544 /note="AluJo repeat: matches 2. .289 of consensus" 'note="AluSc repeat: matches 1. .125 of consensus" /note="MIR repeat: matches 47. .147 of consensus" 7584. .7643 9893. 19948 note="MADE1 repeat: matches 5. .80 of consensus" 8711. .8799 \Tag{note="MIR repeat: matches 59. .145 of consensus" .208 of consensus" /note="16 copies 2 mer ac 100% conserved" 11352. .11558 7584. .7643-recut: macches 47. .147 of c /note="30 copies 2 mer gt 96% conserved" 7969. .8079 /note="L2 repeat: matches 2580. 6304. .6577 'note="AluSx repeat: matches 9. 19272. .19892 /note="L2 repeat: matches 1452. match: GSS: Em:AQ484379" 7969. 8079 /note="MIR repeat: matches 28. 8265. 8544 'note="match: GSS: 21581. .21650 11255. .11286 9753. .9893 /note="AluY 10697.

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where oil retainces are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP: Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl0 RP11-17G2 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence is not the entire insert of clone RP11-1762 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-1762 is at 56701 in this sequence. The true right end of clone RP11-397115 is at 2000 in this
                           humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On or before Jul 12, 2001 this sequence version replaced gi:7381811, gi:13396759.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
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/note="MBR1B repeat: matches 1. .285 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6293. .6521 --row. matches 5. .95 of consensu:
/note="MIR repeat: matches 9. .234 of consensus"
8688. .8929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .218 of
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//note="L2 repeat: matches 2580. .2615 of 61 1305. .1352

//note="24 copies 2 mer ga 75% conserved" complement(2038. .2454)
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/note="MER20 repeat: matches 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER91A repeat: matches 5. 6293. .6521
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1. 56701
/organism="Homo saplens"
/db_xref="taxon:9606"
/chromosome="10"
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/clone_lib="RPCI-11.1"
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                                                                COMMENT
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// Octe="LTRZ2 repeat: matches 413. .509 of consensus"
23148 . .23417

// Octe="LTRZ2 repeat: matches 38. .312 of consensus"
23454 . .23569

// Octe="LTRZ2 repeat: matches 2005. .2146 of consensus"
// Acte="MIR repeat: matches 61. .243 of consensus"
// Acte="MIR repeat: matches 61. .243 of consensus"
// Acte="MIR repeat: matches 215. .3045 of consensus"
// Acte="LIMEC repeat: matches 215. .3045 of consensus"
// Acte="Limec repeat: matches 2151. .3045 of consensus"
// Acte="matche" complement(26913. .27340)
// Acte="matche" complement(26913. .27340)
// Acte="Mir repeat: matches 4. .346 of consensus"
// Acte="Limec repeat: matches 7250. .7739 of consensus"
// Acte="Limec repeat: matches 7250. .7739 of consensus"
// Acte="Mir repeat: matches 6. .390 of consensus"
// Acte="matche 658: Em:AQ735362"
// Acte="matche 658: Em:AQ735362"
// Acte="matche 658: Em:AQ735362"
// Acte="Mir repeat: matches 102. .387 of consensus"
// Acte="Alugh repeat: matches 102. .387 of consensus"
// Actes="Alugh repeat: matches 102. .387 of consensus"
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Human DNA sequence from clone RPI1-17G2 on chromosome 10, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (03-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
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                                                                            /note="12 repeat: matches 2574. .2687 of consensus" 34633. .35136 /note="MENS repeat: matches 1. .511 of consensus" 36692. .37186
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100.0%; Pred. No. 8.8e+02;
iive 0; Mismatches 0;
                        22304. .22755
/note="match: GSS: Em:AQ357726"
'note="match: GSS: Em:AQ714858"
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/note="MIR repeat: matches 6.
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// Acce="Wire repeat: matches 2284. .2534 of consensus" note="Mire repeat: matches 70. .248 of consensus" note="Mire repeat: matches 377. .568 of consensus" note="Mire repeat: matches 337. .568 of consensus" note="Lize repeat: matches 2129. .2318 of consensus" note="Lize repeat: matches 1299. .2318 of consensus" note="Mire repeat: matches 2129. .2318 of consensus" note="Mire repeat: matches 11. .341 of consensus" note="Mire repeat: matches 18. .178 of consensus" note="Mire repeat: matches 18. .178 of consensus" note="Lize repeat: matches 2242. .2521 of consensus" note="Lize repeat: matches 2242. .2521 of consensus" note="Lize repeat: matches 2596. .2708 of consensus" note="Lize repeat: matches 2596. .2708 of consensus" note="Licopies 26 mer 62% conserved" note="Licopies 4 mer ggaa 81% conserved" note="Licopies 4 mer ggaa 81% conserved" note="Licopies 4 mer ggaa 81% conserved" note="Mire repeat: matches 22. .214 of consensus" note="Mire repeat: matches 45. .163 of consensus" note="Mire repeat: matches 28. .260 of consensus" note="Mire repeat: matches 5599. .5820 of consensus" note="Mire repeat: matches 55999. .5820 of co
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// Note="MSTA repeat: matches 1. .426 of consensus" 22480. .22596
// Note="MSTA repeat: matches 1. .426 of consensus" 22480. .22743
// Note="match: STS: Em:HS094YH3" 22597. .22638
// Note="10 copies 2 mer ca 92% conserved" 22597. .22638
// Note="MIR repeat: matches 87. .165 of consensus" 22770. .22846
// Note="MIR repeat: matches 1. .200 of consensus" 23508. .23698
// Note="MER repeat: matches 2399. .2748 of consensus" 24368. .24598
// Note="L1 repeat: matches 2399. .2748 of consensus" 24486. .24581
// Note="L1 repeat: matches 2136. .2213 of consensus" 25073. .24581
// Note="MIRTE repeat: matches 1. .371 of consensus" 25073. .25451
// Note="MIRTE repeat: matches 1. .371 of consensus" 25073. .25451
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/note="match: GSS: Em:AQ507252"
26471. .26619
26933. .27097
/note="MEREA repeat: matches 105. .257 of consensus"
/note="MEREA repeat: matches 1. .188 of consensus"
repeat: matches 2284. .2534 of consensus"
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//note="WIR repeat: matches 31. .225 of consensus"
29356. .29488
/note="WER5A repeat: matches 50. .184 of consensus"
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29578. .29664
// note="MIR repeat: matches 82. .175 of consensus"
31386. .31508
31386. .31508
// note="MIR repeat: matches 42. .164 of consensus"
31974. .32354
// note="MLT11 repeat: matches 1. .410 of consensus"
32596. .33013
// note="MLT1 repeat: matches 1. .410 of consensus"
3407. .33823
// note="MLT1 repeat: matches 128. .547 of consensus"
31833. .34015
// note="MIR repeat: matches 50. .251 of consensus"
34122. .34214
// note="MIR repeat: matches 46. .140 of consensus"
35380. .35474
// note="MIR repeat: matches 46. .140 of consensus"
37028. .37195
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DNA encoding novel
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                                                                                                                                                                     December 11, 2002, 12:23:57; Search time 212.5 Seconds (without alignments) 158.965 Million cell updates/sec
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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N. Caneseg_101002;

SIDS2/gcgdata/geneseg/genesegn-embl/NA1980.DAT:*

SIDS2/gcgdata/geneseg/genesegn-embl/NA1981.DAT:*

SIDS2/gcgdata/geneseg/genesegn-embl/NA1981.DAT:*

SIDS2/gcgdata/geneseg/genesegn-embl/NA1983.DAT:*

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SIDS2/gcgdata/geneseg/genesegn-embl/NA1991.DAT:*

SIDS2/gcgdata/geneseg/genesegn-embl/NA2000.DAT:*

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                     5.1.3
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             2185239 seqs, 1125999159 residues
                          version - 2002 (
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Listing first 45 summaries
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ABV50337
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ABK43728
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                     GenCore
Copyright (c) 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
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The present sequence represents a probe for the A457P variant allele of a human norepinephrine transporter gene. The specification a method for succeptibility to sub-optimal norepinephrine transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter gene are useful for gene threapy for modulating norepinephrine transporter in a target cell and treating susceptibility to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, whyertension, heart disease, psycho stimulant abuse e.g. cocaine or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed sequence tag; secreted protein; cDNA isolation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
 particularly orthostatic intolerance in a subject by detecting a
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 15; DB 22;
100.0%; Pred. No. 4.1e+02;
ive 0; Mismatches 0;
                   polymorphism of norepinephrine transporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein 5' EST, SEQ ID NO: 13316.
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 0 A; 8 C; 1 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; chromosome mapping; ss.
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                                                      Claim 15; Page 69; 133pp; English.
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                                                                                                                                                                                                                                                                                                                                                               amphetamine abuse.
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cancer has metastasized in a patient;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
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                                                                                                                                                                                            Length 352;
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                                                                                                                                                         Sequence 352 BP; 111 A; 73 C; 97 G; 69 T; 2 other;
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0
                                                                                                                                                                                            Score 15; DB 21;
Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate expression marker cDNA 50328,
                                                                                                                                                                                                                              Mismatches
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                                                                                                                         expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                            100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                              ABV50337 standard; cDNA; 445
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
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                                                                                                                                                                                                                              15; Conservative
                                                                                                                                                                                                                                                                               149 CCTTCTCCCCTGTT 135
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Best Local Similarity
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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07-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in claspositics, forensics, gene mapping, identification of mutations in casposible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
         (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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0
                                                                                        Length 445;
                                                                                                                       Indels
                                             Sequence 445 BP; 109 A; 118 C; 109 G; 107 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #1856.
                                                                                  Score 15; DB 23;
Pred. No. 4.3e+02;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 1856; 103pp; English.
                                                                                                                                                                                                                                                                                           AAS66052 standard; cDNA; 549 BP.
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100.0%;
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23-AUG-2000; 2000US-0649167.
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                                                                  Query Match
Best Local Similarity 100...
has 15; Conservative
                                                                                                                                                                            370 CCTTCTCCCCTGTT 384
                                                                                                                                                              1 CCTTCTCCCCCTGTT 15
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                                                                                                                                                                                                                                                                                                                                 AAS66052;
                                                                                                                                                                                                                                                        RESULT 4
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The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comptrises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a journal comprises at least 15 nucleotides and the compination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the chall-length cDNAs and primers and low obtaining of the full-length cDNAs and the primers and sequences; AAH13318 and AAH13333 to AAH18742 represent human cDNA sequences; AAH3346 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                Gaps
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Otsuki T;
                                                                                                                                                ö
                                                                        Length 549;
                                                                                                                                                Indels
Sequence 549 BP; 114 A; 178 C; 140 G; 117 T; 0 other;
                                                                    100.0%; Score 15; DB 23; 100.0%; Pred. No. 4.3e+02;
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A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA clone (5'-primer) SEQ ID NO:886.
                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T, Nishikawa T,
, Sugiyama T, Wakamatsu
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AAH04051/c
ID AAH04051 standard; cDNA; 827 BP.
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99JP-0300253.
2000JP-0118776.
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2000JP-0241899
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                                                                                                                                                Conservative
                                                                                                                                                                                                                                                      423 CCTTCTCCCCTGTT 437
                                                                                                                                                                                                                1 CCTTCTCCCCTGTT 15
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                                                                Query Match
Best Local Similarity
Matches 15; Conserv
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09-JUN-2000;
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represent oligonucleotides, all of which are used in the exemplification

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Gaps

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The present invention describes primer sets for synthesising 5602 [11]—length cDNAs defined in the specification. Where a primer set comprises: (a) an Oilgo-dr primer and an Oilgonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprising a sequence complementary to the oligonucleotide comprising a sequence complementary to the comprises an oilgonucleotide comprising a sequence complementary to the sequence and an oilgonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence, where the comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in c. the specification. The primer sets can be used in antisense therapy and c. the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by che full-length cDNAs. The primers are also useful for the conna and/or diagnosis of the abnormality of the proteins encoded by cDNAs easily without any specialised methods. AAH13628 and AAH13633 to AAH18742 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                  Length 827;
                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito K, Y, Otsuki T;
                                          Sequence 827 BP; 264 A; 138 C; 199 G; 223 T; 3 other;
                                                                                                                          ;
                                                                              Query Match 100.0%; Score 15; DB 22; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 15; Conservative 0; Mismatches 0;
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Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA sequence SEQ ID NO:13660
                                                                                                                                                                                                                                                                                                     AAH15437 standard; cDNA; 1689 BP.
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11-JAN-2200; 2000JP-0118776.
02-MAY-2000; 2000JP-018776.
09-JUN-2000; 2000JP-0241899.
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  of the present invention.
                                                                                                                                                                                   123 CCTTCTCCCCTGTT 109
                                                                                                                                                              1 CCTTCTCCCCTGTT 15
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Yamamoto

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a variant norepinephrine transporter. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to obtain the subject to sub-optimal norepinephrine transport.
                                                                                                                                                                                                                                                                                                                                                                                                         Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine; amphetamine abuse; ss.
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                                                                                                                   Gaps
                                                                                                                  0;
                                                                                  Length 1689;
                                                                                                                                                                                                                                                                                                                                                                         DNA encoding human norepinephrine transporter variant A457P.
                                                                                                                  Indels
                                               Sequence 1689 BP; 555 A; 309 C; 366 G; 459 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "norepinephrine transporter"
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                                                                               100.0%; Score 15; DB 22;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymorphism of norepinephrine transporter gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                   AAH28083 standard; cDNA; 1854
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2000US-0175456.
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               of the present invention.
                                                                                                                Conservative
                                                                                                                                                                     123 CCTTCTCCCCCTGTT 109
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/*tag=
                                                                                                                                                   1 CCTTCTCCCCCTGTT 15
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P-PSDB; AAB84533.
                                                                               Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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11-JAN-2000;
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                                                                                                                                                                                                                                    RESULT 7
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SXSS
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us-09-750-609-10.rng

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WO200155318-A2.
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                                                                                                                                                  ABK43728;
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                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
                                    Gaps
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                                0;
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   Length 1854;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "norepinephrine transporter"
                                                                                                                                                                                                                                                                                 DNA encoding human norepinephrine transporter variant.
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100.0%; Score 15; DB 22; 100.0%; Pred. No. 4.4e+02;
                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 43; Page 119-121; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                             AAH28087 standard; cDNA; 1854 BP.
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11-JAN-2000; 2000US-0175456.
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                                                                                                                                                                                                                                                (first entry)
                                                                                1362 CCTTCTCCCCTGTT 1376
Ouery Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                 1 CCTICTCCCCTGTT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                                                                                                                                                                                 amphetamine abuse; ss.
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hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; ADS; occular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kinney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                                                                                                                                                           Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                     DNA encoding novel central nervous system protein #308.
                                                                               ABK43728 standard; cDNA; 2159 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0186350.
2000US-0189874.
2000US-0190076.
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2000US-0205515.
2000US-0209467.
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2000US-0215135.
2000US-0216647.
2000US-0216880.
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2000US-0220963.
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2000US-0224519
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            1362 CCTTCTCCCCCTGTT 1376
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25-SEP-2000;
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17-NOV-2000;
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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include cutchimmune diseases e.g. rheumatoid arthritis, hyperproliferative cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, cadenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes cad pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders e.g. nonallergic rhinitis, renal disorders e.g. respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cute kidney failure and blood related disorders e.g. myocardial conference transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used to aid wound healing and primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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200005-0251988.
200005-025719.
200005-0251479.
200005-0251856.
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2000US-0249218
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P-PSDB; AAU87398.
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are cisclated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, altergies, autoimmune chaemalytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
                                                                                                                                                                  Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibeterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 1036; 2081pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cand on orid sequences AAS6419-AAS94564 represent novel human DNA and when the common of the invention.
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                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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                                                                                                                                                             DNA encoding novel human diagnostic protein #19092.
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100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0;
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             AAS83288 standard; cDNA; 2451 BP
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23-AUG-2000; 2000US-0649167.
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                                                                                                                (first entry)
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15 - SEP - 2000;

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13-OCT-2000;
13-OCT-2000;
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14-SEP-2000;
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Central nervous system: CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; renal disorder; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                         DNA encoding novel central nervous system protein #584
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2000US-0224518
2000US-0224519.
2000US-0225213.
2000US-0225264.
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2000US-0226681.
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2000US-0227009.
2000US-0228924.
2000US-0229287.
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2000US-0217487.
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2000US-0214886
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2000US-0232080
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      (first entry)
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14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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23-AUG-2000;
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02 - MAR - 2000;
16 - MAR - 2000;
11 - MAR - 2000;
18 - MAY - 2000;
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30 - JUL - 2000;
07 - JUL - 2000;
07 - JUL - 2000;
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26.JUL-2000;
14.AUG-2000;
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14.AUG-2000;
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    05-JUN-2002
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2000US-0249214

2000US-0249218

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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded to novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a madical conditions and in diagnossis of a pathological condition. Disorders which are diagnosed or treated include autolimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, carebrovascular disorders e.g. cardiac arrest, carebrovascular disorders e.g. cardiac arrest, carebrovascular disorders e.g. daylured immunodeficiency virus (AIDS) and fundi, ocular disorders e.g. captulred immunodeficiency virus (AIDS) and fundi, ocular disorders e.g. or corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system of sorders e.g. testicular feminisation, endocrine disorders e.g. disorders e.g. cardiactory disorders e.g. molignancies, cand pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, ceptihelial cell proliferation, to prevent skin aging due to sunburn, to acute kidney failure and blood related disorders e.g. molocardial infarction. The polypeptides can also be used to aid wound healing and epithelial organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotraxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capaballities, fat content, lipid, protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein clone as180_1 nucleotide sequence SEQ ID NO:159.
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                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 594; 837pp; English.
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                                                                                                                                                                                                                                                                                                             Ruben SM;
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2000US-0251479.
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2000US-0251989.
2000US-0251990.
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                                    2000US-0251030
2000US-0251988
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                                                                                                                                                                                                                                                                                                             Rosen CA, Barash SC,
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les 15; Conserv
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AAA16618 to AAA16697 encode the human secreted proteins given in AAV94898 to AAV94980, isolated from human adult brain, adult thyroid, adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult placenta, adult testis, whole embryo, adult cartilage, Kidney, adult placenta, adult thymus, foetal placenta, adult uterus, adult tumour, and adult bladder, CDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable of predicted to have biological activities which would make them suitable of the protein is preferentially expressed, as molecular weight on animals. The polynucleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight chromosomes or to map gene positions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined immunedeficiency (SID), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency virus (HIV), hepatitis, herpesviruses, mycobacteria, Leismania spp., malaria and candidiasis. The proteins can be used to treat autoimmune disorders such
                        infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; rheumatoid arthritis; autoimmune pulmonary inflammation; asthma; Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis; insulin dependent diabetes mellitus; graft-versus-host-disease; autoimmune inflammatory eye disease; allergy; ss.
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Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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severe combined immunedeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collins-Racie LA, Evans C;
Steininger RJ, Spaulding V;
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I, Agostino MJ,
Fechtel K;
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antithyroid; immune deficiency;
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99US-0119931.
99US-0120575.
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98US-0099229.
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99US-0096622
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Matches 15; Conservative
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Clark HF,
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P-PSDB; AAY94977.
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                                                                                                                                                                                                                                                                  Homo sapiens.
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Wong GG,
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(first entry)

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ABV22746 standard; cDNA; 4215 BP.
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                                                                                   ABV22746;
                             RESULT 15
ABV22746/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. thrombocytopaenia), inflammatory alsorders (e.g. asthma), neurodegenerative disorders (e.g. hemophilia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABR35610-ABR36232 represent the cDNA sequences of the invention that encode for novel human
                                                                                                                                                                                                 Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collins-Racie LA, Evans C;
Bowman MR, Spaulding V, Wong GG;
esnick RJ, Gulukota K, Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 15; DB 24; Length 3580; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                         cDNA sequence #21 encoding novel human secreted protein.
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Howes SH, Resnick RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 85-86; 393pp; English.
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                                                                                          ABK35630 standard; cDNA; 3580 BP.
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                                                                                                                                                (first entry)
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              2528 CCTTCTCCCCTGTT 2542
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Best Local Similarity 100.
Matches 15; Conservative
1 CCTTCTCCCCTGTT 15
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Clark HF, Fechtel K,
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                                                                                                                                                                                                                                                                                                                WO200177289-A2.
                                                                                                                                              08-MAY-2002
                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                           18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobs K,
                                                                                                                      ABK35630;
                                                                 RESULT 14
                                                                                ABK35630/
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                                                     Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (e) selecting a composition for inhibiting prostate cancer in a patient;(f) assessing the prostate cell carcinogenic potential of a compound;(g) determining whether prostate cancer has metastasized in a patient;(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid molecule (I) compa nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4215 BP; 1325 A; 808 C; 818 G; 1251 T; 13 other;
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100.0%; Score 15; DB 23; ? ...
100.0%; Pred. No. 4.5e+02; ...
100.0%; Pred. No. 4.5e+02; ...
prostate expression marker cDNA 22737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 4005-4006; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 11, 2002, 13:38:16 Job time : 213.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monahan JE;
                                                                                   pharmacogenomic marker; gene; ss.
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2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                                                                                                                                                                               WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-2000; 2
18-JUL-2000; 2
13-DEC-2000; 2
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                                                                                                                                            Homo sapiens
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25-MAY-2000;
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Gaps

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1053 CCTTCTCCCCTGTT 1039

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1 CCTTCTCCCCCTGTT 15

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GenCore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:29:32; Search time 47 Seconds

(without alignments)

97.876 Million cell updates/sec

Title: US-09-750-609-10

Perfect score: 15
Sequence: 1 ccttctcccctgtt 15
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/pcrtus_comb.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Issued_Patents_NA:*

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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 11, Appl Sequence 747, App Sequence 54, Appl Sequence 54, Appl	9, A 1, A 2, A 3, A	2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	11, 12, 13, 14, 12, 13, 14, 14, 14, 14, 14, 14, 14, 14, 14, 14	Sequence 12, Appl Sequence 101, App Sequence 1, Appli Sequence 1, Appli
SUMMARIES	US-09-502-653-11 US-09-605-785-747 US-08-975-316-54 US-08-975-192A-54 US-08-615-192A-54	US-09-615-192A-55 US-08-482-746-9 US-08-381-433A-1 US-08-331-433A-3 US-09-258-373-21	US-08-379-496-1 US-08-484-044-11 US-08-965-729A-2 PCT-US93-03077-2 US-08-965-729A-1	-08-244-189-1 -08-306-691B- -09-821-736-1 -08-770-301A- -09-175-581-2 -09-330-330-3	US-09-078-294-12 US-08-742-185-101 US-08-996-306-1 US-09-338-907-1
DB	44040	144110	11454	・1142544	4624
Length	735 738 1074 1074	1075 1374 1514 1626 1875	101 101 101 101 101 101		18073 43795 56516 56516
% Query Match	88 88 88 88 88 88 88 88 88 88 88 88 88		6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		88 89 9.3 89 9.3 89 9.3
Score	4.4.4.4.4	. <b></b>	4.4.4.4.4.6.1.1.1.1.1.1.1.1.1.1.1.1.1.1.	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	13.4 13.4 13.4
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Gaps

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Length 735; Indels

Score 13.4; DB 4; Pred. No. 2.7e+02; 0; Mismatches 1;

Query Match 89.3%; Best Local Similarity 93.3%; Matches 14; Conservative (

Qy Db RESULT 2
US-09-605-785-747/c
Sequence 747, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:

28 13.4 89.3 56516 4 US-09-218-207-179 29 13.4 89.3 56520 4 US-09-218-207-179 30 13.4 89.3 56520 4 US-09-384-116-3 31 13.4 89.3 65620 4 US-09-784-116-3 32 13.4 89.3 65642 4 US-09-784-116-3 32 13.4 89.3 65742 4 US-09-784-116-3 33 13.4 89.3 65742 4 US-09-784-116-3 34 13.8 86.7 1005 4 US-09-255-744A-1 2 36 13 86.7 2873 1 US-08-619-695-8 39 13 86.7 2873 1 US-08-149-695-8 39 13 86.7 2873 1 US-08-149-695-1 41 13 86.7 2873 1 US-08-137-228-1 41 13 86.7 2873 1 US-08-137-228-1 41 13 86.7 2873 1 US-09-137-228-1 42 13 86.7 2873 1 US-09-137-228-1 43 12.4 82.7 2873 1 US-09-99-7-90B-20 58quence 11, Application US/09502653 59quence 11, Application US/09502653 5quence	Sequence 179, App Sequence 179, App Sequence 3, Appli Sequence 1, Appli Sequence 29, Appli Sequence 29, Appli Sequence 1, Appli Sequence 8, Appli Sequence 8, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli		shown in SEQ ID
28 13.4 89.3 56516 6 2 3 13.4 89.3 56520 6 3 13.4 89.3 56520 6 3 13.4 89.3 56520 6 3 13.4 89.3 4411529 3 13.4 89.3 4411529 3 13.4 89.3 4411529 3 13.4 89.3 4411529 3 13.8 6.7 1905 4 3 13 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 86.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7 2687 1 3 8 6.7	09-23 -09-33 -09-72 -09-72 -09-26 -09-29 -09-29 -09-29 -09-29 -09-29 -09-29	n n n n n n n n n n n n n n n n n n n	AC13 (DSM 8721) .he Galactanase
28 13.4 89.3 3 13.4 89.3 3 13.4 89.3 3 13.4 89.3 3 13.4 89.3 3 13.4 89.3 3 13.4 89.3 3 13.86.7 3 13 86.7 3 13 86.7 3 13 86.7 3 13 86.7 3 13 86.7 41 13 86.7 41 13 86.7 42 13 86.7 43 12.4 82.7 44 12.4 82.7 45 12.4 82.7 47 12.4 82.7 48 12.4 82.7 48 12.4 82.7 49.502-653-11/C Sequence 11, Applicate Patent No. 6331426 GENERAL INFORMATION: APPLICANT: Schlein, APPLICANT:	56516 56520 65042 411529 776 11905 2687 2687 2887 2887 2887 2887 2887 2887	us/C s s Es roth in in in in in in in in in in in in in	agaradhaer ) DNA encodi NO.12.
28 13.4 29 13.4 39 13.4 31 13.4 31 13.4 32 13.4 33 13.4 33 13.4 34 13.4 34 13.4 44 12.4 44 12.4 44 12.4 44 12.4 44 12.4 44 12.4 45 12.4 45 12.4 47 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.4 48 12.	•	1/c Applicat 31426 31426 31426 Amarion I ausen, chlein, Lis ech, Lis ech, Lis chlein I boll I boll I boll I carion I CATION I CAT	cillus ss )(735 ATION: ATION:
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	00000000000000000000000000000000000000	8 - 8 - 6	; TYP] ; TYP] ; ORG, ; FEA, ; LOC, ; OTH] ; OTH]

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Score 13.4; DB 2;
Pred. No. 2.8e+02;
0; Mismatches 1;
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Pred. No. 2.8e+02;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                 REFERENCE/POCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-615-192A-54/c; Sequence 54, Application US/09615192A; Patent No. 6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 55, Application US/08975316; Patent No. 5952486; GENERAL INFORMATION:
                   37,007
                                                                                                                                                                                                                                                                                    89.3%;
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                                                                                                                               INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                    Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                         TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                               1 CCTTCTCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCTTCTCCCCCTGTT 15
               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA; ORGANISM: Pinus radiata
US-09-615-192A-54
                                                                                                                                                                                                                              linear
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Best Local Similarity
Matches 14; Conserv
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US-08-975-316-54
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                                                                                                                                                                                                                                                                APPLICANT: Wang, Aljun Skeiky, Yasir A.W.
APPLICANT: Replet, Villiam APPLICANT: Heplet, Villiam APPLICANT: HEPLE CANOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 54, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
BAPPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GEIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.4; DB 4; Length 7 Pred. No. 2.7e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 21011.42701.0 FROSIDILE CURRENT APPLICATION NUMBER: US/09/605,785 CURRENT FILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 835 SSO ID NO 747 LENGTH: 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(738)
; OTHER INFORMATION: n=A,T,C or G
US-09-605-785-747
u, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
                                                                       Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
                                                             Harlocker, Susan L.
                                                                                                                                   Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.3%;
Best Local Similarity 93.3%;
Matches 14; Conservative
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ZIP: 98121
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                    Li, Samuel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
                                       APPLICANT
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Gaps
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APPLICANT: and GRIERSON, Alastair W.
IITLE OF INVENTION: MATERIALS AND METHODS FOR
IITLE OF INVENTION: THE MODIFICATION OF PLANT LIGHIN CONTENT
Length 1074;
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Madification of Plant Lignin Content
FILE REPERENCE: 11000-11035-409/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR PAPLICATION NUMBER: US 08/713,000
PRIOR PAPLICATION NUMBER: US 08/713,000
PRIOR PELING DATE: 1996-09-11
PRIOR PELING DATE: 1996-09-11
PRIOR PELING DATE: 1996-09-11
PRIOR PELING DATE: 1998-10-09
NUMBER OF SEC ID NOS: 405
NUMBER OF SEC ID NOS: 405
SOFTWARE: FASTERO for Windows Version 3.0
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                                                             Indels
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Score 13.4; DB 4; Length 1374;
Pred. No. 2.8e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                   APPLICANT: Lewis, Kuthy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Sawchendson, Cynthia J.
APPLICANT: Sawchendson, Cynthia J.
TITLE OF INVENTION: CLoning and Recombinant Production of
TITLE OF INVENTION: CRE Receptor(s)
FILE REFERENCE: P41-90002
CURRENT APPLICATION NUMBER: US/08/482,746B
CURRENT FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-01-17
EARLIER APPLICATION NUMBER: US 08/374,009
EARLIER FILING DATE: 1994-05-25
EARLIER FILING DATE: 1994-05-25
EARLIER FILING DATE: 1994-05-25
EARLIER FILING DATE: 1993-08-23
EARLIER APPLICATION NUMBER: US 08/110,286
EARLIER FILING DATE: 1993-08-23
SARRIER APPLICATION NUMBER: US 08/079,320
EARLIER FILING DATE: 1993-06-18
NUMBER OF EQ. ID NOS: 15
SOFFWARE: FRASER PARSER FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lovenberg, Timothy W.
APPLICANT: Lovenberg, Timothy W.
APPLICANT: Lovenberg, Tilman
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: DeSouza, Errol B.
TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
TITLE OF INVENTION: RECEPTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSED: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                      5-08-482-746-9
Sequence 9, Application US/08482746B
Patent No. 6399315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08381433A Patent No. 5786203 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.3%;
93.3%;
                                                                                                                                                                                  APPLICANT: Perrin, Marilyn H. APPLICANT: Chen, Ruoping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1080 cerecreceerar 1094
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (79)...(1371)
US-08-482-746-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-381-433A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55, Application US/09615192A

Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content;
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 2.8e+02;
); Mismatches 1;
                                                                                                                              IBM Compatible
SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                         CURRENT APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION NUMBER: US/08/975,316
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY AGENT INFORMATION:
NAME: SLEATH, Janet
RECISTATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECATION 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1075 base pairs
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                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 93.3
Matches 14; Conservative
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STRANDEDNESS: single
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CORGANISM: Pinus radiata
US-09-615-192A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 14; Conserve
                                                                                                                            COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
STATE: WA
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                                                               98121
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SEQ ID NO 55
LENGTH: 1075
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Patent No. 5593833
GENERAL INFORMATION:
APPLICANT: MORRISON, Nigel A
APPLICANT: EISMAN, John A
APPLICANT: KELLY, Paul J
TITLE OF INVENTION: Assessment of Trans-Acting Factors Allelic
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                 Length 1626;
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                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09258373
Sequence 21, Application US/09258373
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Aiao, Sheng
TITLE OF INVENTION: HMGI(Y)-LAMA4* FUSION ONCOGENE,
TITLE OF INVENTION: HMGI(Y)-LAMA4* FUSION ONCOGENE,
TITLE OF INVENTION: ONCOPROTEIN AND METHODS OF USE
FILE REFERENCE: B0801/7135/ERP
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 60/076,401
EARLIER FILING DATE: 1998-02-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                             Score 13.4; DB 1;
Pred. No. 2.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.4; DB 3;
Pred. No. 2.9e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIN Release #1.24
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/379,496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 89.3%;
Best Local Similarity 93.3%;
Matches 14; Conservative
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93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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ORGANISM: Homo Sapiens
US-09-258-373-21
                                     linear
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               STRANDEDNESS:
TOPOLOGY: lin
FEATURE:
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                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 21
LENGIH: 1875
                                                                                                                       US-08-381-433A-3
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US-09-258-373-21
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Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lovenberg, Timothy W.
APPLICANT: Oltersdorf, Tilman
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: DeSouza, Errol B.
TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
TITLE OF INVENTION: RECEPTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,433A
FLING DATE: 31-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: MCMSters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 690068.401C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: 723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 3:
                                                                           ATTORNEY AGENT INFORMATION:
NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 690068.401C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELERA: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARATERISTICS:
LENGTH: 1514 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,433A
FILING DATE: 31-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08381433A Patent No. 5786203 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1626 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 1045 CCTCCTCCCCCTGTT 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCTTCTCCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 44..1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-381-433A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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Gaps

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Sequence 2, Application US/08965729A
Patent No. 6200751
GENERAL INFORMATION:
APPLICANT: Jan-Ming Gu and Charles T. Esmon
TITLE OF INVENTION: ENDOTHELIUM SPECIFIC EXPRESSION
TITLE OF INVENTION: REGULATED BY EPCR CONTROL ELEMENTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: /note= "Nucleotides 2272 through 2729 are
OTHER INFORMATION: thrombin responsive element"; Human
                                Score 13.4; DB 1; Length 3182;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.3%; Score 13.4; DB 4; Length 3224; 93.3%; Pred. No. 3e+02; 1; Indels 0
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/965,729A FILING DATE: O7-NOV-1997 CLASSIFICATION:
                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,718
FILING DATE: 08-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 164 PCT
TELECOMMUNICATION INFORMATION:
TELECHONE: 404-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9303077 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 3224 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                89.3%;
93.3%;
                                                    Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 2759 CCTTCTCCCCCTTTT 2773
                                                                                                                                                 414 CCTTCTCCCTTGTT 428
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                                                                                                                     1 CCTTCTCCCCTGTT 15
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 30309-4530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GA
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                                  Query Match
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APPLICANT: Fu, Ying-Hui
APPLICANT: Friedman, David L.
APPLICANT: Friedman, David L.
APPLICANT: Friedman, David L.
APPLICANT: Forwick, Raymond G.
APPLICANT: Fenwick, Raymond G.
TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                  Length 2169;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,044
                                                                                                                                                                                                                                                                                                                                                                                  Score 13.4; DB 1;
Pred. No. 2.9e+02;
); Mismatches 1;
FILING DATE: 02-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BATDARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-114
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 783-6040
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2169 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/019,940
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUBBER: D-5443
TELECOMMUNICATION:
TELEPHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08484044 Patent No. 5552282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-484-044-11
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 CCTTCTCTCCCTGTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCTTCTCCCCTGTT 15
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CLASSIFICATION: 435
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APPLICANT: Caskey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Houston STATE: Terri
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US-08-484-044-11
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Patent No. 6200751

GENERAL INFORMATION:
APPLICANT: Jian-Ming Gu and Charles T. Esmon
TITLE OF INVENTION: REGULATED BY EPCR CONTROL ELEMENTS
TITLE OF INVENTION: REGULATED BY EPCR CONTROL ELEMENTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrae L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Pred. No. 3e+02;
0; Mismatches 1; Indels 0
APPLICANT: Board of Regents, The Universityof Texas System APPLICANT: Gaynor, Richard B. APPLICANT: Gaynor, Richard B. TITLE OF INVENTION: REGULATING GENE EXPRESSION TITLE OF INVENTION: REGULATING GENE EXPRESSION
                                                                                                                                                                                                                                                                 ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/03077
FILING DATE: 19930331
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UTFD270PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/862,025
FILING DATE: April 2, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                    ADDRESSEE: Arnold White & Durkee STREET: P.O. Box 4433
CITY: Houston STATE: Texas COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kammerer, Patricia A. REGISTRATION NUMBER: 29,775 REFRENCE/DOCKET NUMBER: UTFD TELECOMMUNICATION INFORMATION: TELEFHONE: 713-787-1540 TELEFAX: 713-749-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 3279 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCTTCTCCCCTGTT 15
                                                                                                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GA
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US-08-965-729A-1
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PRILICATION NUMBER: US/08/965,729A
FILING DATE: 07-NOV-1997
FLING DATE: 08-NO-1097
PRIOR APPLICATION NUMBER: US 60/030,718
FILING DATE: 08-NOV-1997
ATTORING DATE: 08-NOV-1997
ATTORING DATE: 08-NOV-1997
ATTORING DATE: 08-NOV-1997
ATTORING DATE: 08-NOV-1997
TELEPHONE: 13.24
FREERENEL/COCKET NUMBER: OMR 164 PCT
FELEPHONE CHRAPATERISTICS: 18-NOV-1997
TELEPHONE: 08-NOV-1997
TELEPHONE: 10-NOV-1997
TOPOLOGY: 11-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-1-18-NOV-18
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GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:35:52; Search time 52.5 Seconds

(without alignments)

111.409 Million cell updates/sec

Title: US-09-750-609-10

Perfect score: 15
Sequence: 1 ccttctcccctgtt 15
Sequence: 1 ccttctcccctgtt 15
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 2000000000
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Published_Applications_NA:*

1. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

2. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

2. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

3. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

4. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

5. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

6. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

7. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

8. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

9. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

10. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

11. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

12. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

13. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

13. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

14. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

14. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

14. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

14. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

14. \cgn2_6\ptodatta/2\ptubpna\USO_PUBCOMB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query No. Score Match Length DB ID  1																					
Score Match Length DB II 15 100.0 15857 10 14 93.3 389 10 14 93.3 493 10 14 93.3 493 10 14 93.3 493 10 14 93.3 493 10 14 93.3 493 10 13.4 89.3 16877 10 13.4 89.3 264 10 13.4 89.3 401 9 U 13.4 89.3 401 9 U 13.4 89.3 401 9 U 13.4 89.3 401 10 13.4 89.3 401 10		Description	Sequence 1704, Ap	Sequence 1577, Ap	Sequence 3234, Ap	Sequence 84, Appl	Sequence 1570, Ap	Sequence 13104, A	Sequence 1692, Ap	Sequence 3063, Ap	Sequence 3349, Ap	Sequence 4063, Ap		Sequence 96, Appl	Sequence 10470, A	Sequence 1267, Ap	Sequence 1268, Ap	Sequence 1269, Ap	Sequence 1267, Ap		
Score Match Length DB II 15 100.0 15857 10 14 93.3 389 10 14 93.3 493 10 14 93.3 493 10 14 93.3 493 10 14 93.3 493 10 14 93.3 493 10 13.4 89.3 16877 10 13.4 89.3 264 10 13.4 89.3 401 9 U 13.4 89.3 401 9 U 13.4 89.3 401 9 U 13.4 89.3 401 10 13.4 89.3 401 10				,																	
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SCOOPE 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		DB	10	10	10	σ	10	10	10	10	10	10	10	6	10	0	6	σ	10	10	10
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	æ	Query Match	100.0	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	89.3	89.3	89.3	89.3	89.3	89.3	89.3	89.3	89.3	89.3
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1267, 1268, 1268, 1269, 1269, 1100, 1100, 1134,	3, 1 83777	Sequence 703, App Sequence 298, App
US-09-795-686-1267 US-09-795-686-1268 US-09-954-531-332 US-09-954-531-332 US-09-954-531-555 US-09-954-456-1100 US-09-954-456-1700 US-09-954-456-1784 US-09-964-766A-134 US-09-964-761-551	US-09-917-800A-701 US-09-759-149-747 US-09-822-827-747 US-09-822-827-747 US-09-925-301-438 US-09-191-724-9 US-09-981-401-1 US-09-981-401-1 US-09-981-401-3 US-09-981-401-3 US-09-974-298-101-3 US-09-974-298-101-3 US-09-974-298-101-3 US-09-974-298-101-3	US-09-938-842A-703 US-09-864-864-298
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## ALIGNMENTS

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APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
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         Sequence 1704, Application US/09764864
Patent No. US20020132753A1
GREEAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 15; DB 10; 100.0%; Pred. No. 94;
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-954-456-1577/c
US-09-764-864-1704
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FALENT NO. USJOURNATION:
APPLICANT: Salceda, Susana
APPLICANT: Racion, Roberto
APPLICANT: Recipon, Herver
APPLICANT: Recipon, Herver
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and
FILE REFERENCE: DEX-0277
CURRENT APPLICATION NUMBER: US/10/001,835
CURRENT APPLICATION NUMBER: 60/249,997
PRIOR APPLICATION NUMBER: 60/249,997
PRIOR APPLICATION NUMBER: 60/249,997
NUMBER OF SEQ ID NOS: 228
SOFTWARE: Patentin Version 3.1
SEQ ID NO 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-833-381-1570/c
Sequence 1570, Application US/09833381
Sequence 1570, Application US/09833381
Sequence 1570, Application US/09833381
Sequence 1570, Application US/09833381
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE REPRENCE: 5800-119
CURRENT FILING DATE: 2001-04-11
PRIOR PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1570
LENGTH: 493
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                                                                                                                      Sequence 84, Application US/10001835
Patent No. US20020160387A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(493)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1570
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Best Local Similarity 93.3
Matches 14; Conservative
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296 CCTTCTCCCCTGT 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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CORGANISM: Homo sapien
US-10-001-835-84
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US-09-864-761-13104
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Sequence 3234, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Scherf, Uwe

APPLICANT: Scherf, Uwe

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US 60/211,379

PRIOR PILING DATE: 2000-06-14

PRIOR PLING DATE: 2000-06-14

SOFTWARE: PALENTING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3234
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                     PRIOR FILING DATE: 2000-03 20
PRIOR FILING DATE: 2000-03-5
PRIOR FILING DATE: 2000-03-5
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SEQ ID NO 1577
LENGTH: 389
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) LOCATION: (1).(389)

) CTHER INFORMATION: n = a or c or g or t

US-09-880-107-3234
     FILING DATE: 2000-09-20
PPLICATION NUMBER: US/60/234,923
FILING DATE: 2000-09-25
APPLICATION NUMBER: US/60/235,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-1577
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Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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Patent No. US20020147140a1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION:

FILE REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper;

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3063

LENGTH: 8894
Sequence 1692, Application US/09764864

Patent No. US20020132753A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ3

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper;

NUMBER OF SEQ ID NOS: 1792

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1692

LENGTH: 8894
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CURRENT FILING DATE: 2001-01-17
(Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3349
LENGTH: 16877
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
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2.7e+02;
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; Patent No. US20020147140A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 14; Conservative
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Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-764-864-1692
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CORGANISM: Homo sapiens
US-09-764-877-3063
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; ORGANISM: Homo sapiens
US-09-764-877-3349
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                                                APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hansel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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100.0%; Pred. No. 2.2e+02;
live 0; Mismatches 0; Indels
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COTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
COTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68
COTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
US-09-864-761-13104
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13104
EBNGTH: 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00664
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR PELICATION NUMBER: GB 24263.6
PRIOR FILING-DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                       FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00665
FILLING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00663
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PRICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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OTHER INFORMATION: EXPRESSED IN PLACE
OTHER INFORMATION: EXPRESSED IN ADULT
OTHER INFORMATION: EXPRESSED IN FETAL
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Best Local Similarity 100.
Matches 14; Conservative
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  US20020048763A1
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GENERAL INCORMATION:
GENERAL INCORMATION:
SEQUEDER, Sergio H.
APPLICANT: Eisenberg, Bavid
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINED THE FUNCTIONS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: CT/VS00/02246
PRIOR APPLICATION NUMBER: 60/119,531
PRIOR APPLICATION NUMBER: 60/119,531
PRIOR APPLICATION NUMBER: 60/118,206
PRIOR APPLICATION NUMBER: 60/118,206
PRIOR PLING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/118,006
PRIOR PLING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR PLING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
PRIOR PRILING DATE: 1999-11-12
PRIOR PRILING DATE: 1999-11-12
SUPPHYARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Hadong
APPLICANT: Li, Hadong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
                                         Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.4; DB 9; Length 315; Pred. No. 4.1e+02;
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                                           DB 10;
                                         Score 13.4; DB :
Pred. No. 4e+02;
0; Mismatches
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; Sequence 10470, Application US/09783590
; Patent No. US20020110850A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mycobacterium tuberculosis US-09-712-363-96
                                                                                                                                                                                                                                                     US-09-712-363-96/c
; Sequence 96, Application US/09712363
; Patent No. US20020164588A1
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                                           Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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  US-09-783-590-10753
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Fatent No. US2002011085041

GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Li, Haodong
APPLICANT: Li, Haodong
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT PAPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
FRIOR PAPLICATION NUMBER: 08/420,856
FRIDK APPLICATION NUMBER: 08/346,731
FRIDK APPLICATION NUMBER: 08/346,731
FRIDK APPLICATION DATE: 1995-04-11-21
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Pred. No. 3.9e+02;
); Mismatches 1; Indels 0
    Length 16877;
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100.0%; Pred. No. 2.9e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                   Sequence 4063, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bacillus licheniformis US-09-974-300-4063
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93.3%;
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 93.3
Matches 14; Conservative
  Query Match 93.3
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                             Db 1269 CCTTCTCCCCTGT 1256
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US-09-974-300-4063
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LENGTH: 264
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LENGTH: 198
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Score 13.4; DB 9; Length 401;
Pred. No. 4.2e+02;
); Mismatches 1; Indels (
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Pred. No. 4.2e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stefansson, Hreinn APPLICANT: Stefansson, Hreinn APPLICANT: Steinthorsdottir, Valgerdur APPLICANT: Steinthorsdottir, Valgerdur TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1268
                                          APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345_2004_001
CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001_09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001_00-05
PRIOR FILING DATE: 2001_02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1268, Application US/09946807
Patent No. US20020165144A1
GENERAL INFORMATION:
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93.3%;
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93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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      Patent No. US20020165144A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-946-807-1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-1268
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Pred. No. 4.1e+02;
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PRIOR APPLICATION NUMBER: 08/420, 856
PRIOR FILING DATE: 1955-04-12
PRIOR FILING DATE: 1994-11-21
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver: 2.0
LENGTH: 363
                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (47)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                             LOCATION: (102)
OTHER INFORMATION: n equals a,t,g, or NAME/FXY: misc feature
LOCATION: (105)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (352)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (356)
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LOCATION: (112)
OTHER INFORMATION: n equals a,t,g, or
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (123)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (145)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (193)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (193)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
NAMESKEY: misc feature
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Best Local Similarity 93.3%;
Matches 14; Conservative
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LOCATION: (336)
                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: (226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
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US-09-946-807-1267; Sequence 1267, Application US/09946807

RESULT 14

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                   OM nucleic - nucleic search, using sw model
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December 11, 2002, 13:27:12; Search time 1661 Seconds (without alignments) 146.257 Million cell updates/sec 1 cettetececetgtt 15 US-09-750-609-10 15 Title: Perfect score: Sequence: Run on:

IDENTITY_NUC Gapoxt 1.0 Scoring table:

16154066 seqs, 8097743376 residues Searched:

32308132 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* •• Database

em_gss_fun: *
em_gss_mam: *
em_gss_mus: *
em_gss_other: *
em_gss_pro: * em_estba:*
em_esthum:*
em_estin:*
em_estov:*
em_estpl:*
em_estpl:*
em_estro:*
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gb_ests:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ф				
Result		Query				
No.	S	Match		DB	ID	Description
	:	15 100.0	181	17	AZ284882	AZ284882 RPCT-23-
7	15	100.0	226	10	AV335397	AV335397 AV335397
о С	15	100.0	246	6	AL708655	AL708655 DKFZD686
C 4	15	100.0	297	6	AV067076	AV067076 AV067076
S	15	100.0	378	14	F07213	F07213 HSC1ZB021
9	15	100.0	393	14	T08889	T08889 EST06781 ]

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4-1-1

AJ449549 4 T. Druce 2 16070503 2 16070503 3 10070906 3 10070906 3 10070906 3 10070906 4 1008006 4 1008006 5 2 34611470 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	AQ555494 Sheared D BF962681 PM4 -NN120 AQ661274 Sheared D BE875768 601487226 AW556920 EST368990 AJ450711 AJ450711 AJ450718 AJ45078 BI859096 603385158 AJ450146 AJ450146
AJ449549 TA8E07F BAJ3976 AMJ3970 AM50464 BE9511621 BE9511621 BE9511621 BE926996 AM69966 AM69966 AM69376 TA29590 RR24819 BH622376 RR24819 BH622376 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382 AJ446382	
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## ALIGNMENTS

	AZ284882 181 bp DNA linear GSS 27-JUL-2000	RPCI-23-442E20.TV RPCI-23	, DNA sequence.	AZ284882	A2284882.1 GI:9526668	GSS.	house mouse.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 181)	Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret	,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.	and Fraser, C.M.	Mouse BAC End Sequences from Library RPCI-23	Unpublished (1999)	Other_GSSs: RPCI-23-442E20.TJ	Contact: Shaying Zhao	Department of Eukaryotic Genomics	The Institute for Genomic Research	9712 Medical Center Dr., Rockville, MD 20850, USA	Tel: 301 838 0200	Fax: 301 838 0208	Email: szhao@tigr.org	Clones are derived from the mouse BAC library RPCI-23. For BAC	Ilbrary availability, please contact Pieter de Jong	(pieceredejong.med.bulialo.edu). Ciones may be purchased irom
RESULT 1 AZ284882	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS			TITLE	JOURNAL	COMMENT										

FEATURES

ORIGIN

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polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL708655 246 bp mRNA linear EST 22-MAR-2002 DKF2p686J0853_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKF2p686J0853 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6330571M18"
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oblongata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 246)
Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
Est (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Contact: Wambutt R
                                                                                                                       system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 226;
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100.0%; Pred. No. 5.7e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 t
                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                         Location/Qualifiers
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Matches 15; Conserv
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AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-9226
Fax: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI: Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DHIOB electrocompetent cells (BRL Life Technologies).

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Whi.http://genome-gsc.riken.go.jp,
Sasaki,N., Izawa,M., watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/Dac_ends/mouse/Dac_end_intro.html Plate: 442 row: E column: 20 Seg primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcriptional sequencing: A method for DNA sequencing using RNA
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100.0%; Pred. No. 5.5e+03;
ive 0; Mismatches 0;
                                                                                                                                                                                                                       /strain="C57BL/6J"
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                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV335397.1 GI:6375449
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JOURNAL
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AV335397
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KEYWORDS

SOURCE

COMMENT

0

Gaps

; 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 bp mRNA linear EST 20-FEB-1995
HSC12B021 normalized infant brain cDNA Homo sapiens cDNA clone
c-15b02, mRNA sequence.
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//tissue_type="total brain"
//dev_stage="3 months old"
//note="Organ: Drain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
Site_2: NotI; sex=Female; dev_stage=3 months old;
Site_1 = 1 months old;
total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria: Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 378)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single read.

Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-lzb02
Seq primer: (-21)M13_universal.

Location/Qualifiers
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Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 3316947280
Fax: 33160778698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 15; DB 9; Length 297; 100.0%; Pred. No. 6.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="c-1zb02"
/clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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/db_xref="taxon:9606"
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F07213.1 GI:672862
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Best Local Similarity 100.
Matches 15; Conservative
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 297)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
          Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkf2- heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

No s1 sequence available.
                                                                                                                                                                      This clone (DKFZp686J0853) is available at the RZPD in Berlin. Please contact the RZPP: Ressourcentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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                                                                                                                                                                                                                                                                                           1. 246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="orkrap68650853"
/clone=lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH108"
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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/strain="C57BL/6J"
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                                                                                                                                                                                                                                                                     T08889 393 bp mRNA linear EST 03-AUG-1993 EST06781 Infant Brain, Bento Soares Homo sapiens CDNA clone HIBBL71 5' end similar to p87 transporter-like protein, mRNA sequence. T08889 GI:389917
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      Psychiatry
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/cloud_lib="infant Brain, Bento Soares"
/note="Vector: Lafmid; The IB library was constructed by directional cloning and oligo(dr)-priming in the Lafmid vector, utilizing a three month old infant human brain (total brain)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    lafmid BA vector. Clone library from B.Soares, Psychi.
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press" 2 others
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                                                                                                 100.0%; Score 15; DB 14;
100.0%; Pred. No. 6.4e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research 932 Clopper Road, Gaithersburg, MD 20878 Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 393
/organism="Homo sapiens"
/db_xref="ATCC (inhost):85383"
/db_xref="taxon:9606"
/clone="HIBBL71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Email: mdadams@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
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Matches 15; Conservative
                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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TAREO7P 401 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 8e07, forward sequence, genomic
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
rypanosoma brucei (TRE0927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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1 (bases 1 to 401)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CBl0 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Phasianinae; Gallus.

1 (bases I to 399)

Buerstedde, J.M.

Gallus gallus bursal lymphocyte EST

Unpublished (2002)

Contact: Buerstedde JM

Collular Immunology

Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany

Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
78 c 103 g 97 t
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/organism="callus gallus"
/db_xref="taxon:9031"
/clone="22g1r1"
/clone_lib="riken1"
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Trypanosoma brucei
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Homo sapiens
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DEFINITION
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AUTHORS
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KEYWORDS
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                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library constructed by: Chandra Tucker and Gregory Niemi DNA Sequencing Dy: Washington University Genome Sequencing Center Clone distribution: RessourcentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
Seq primer: T3 ET from Amersham
High quality sequence stop: 396.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., and Wilson, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                                                                                           BI706542 403 bp mRNA linear EST 13-FEB-2002 fq07c03.yl Zebrafish adult retina cDNA Danio rerio cDNA clone 4790765 5' similar to TR:Q9UH03 Q9UH03 BK250D10.3;, mRNA sequence.
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/dev_stage="1-2 years"
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/hote="Vector: Lambda ZAP II (pBluescript SK-); Site_1:
ECORI; Site_2: Sall; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number: 760"
                                                        Gaps
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Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fal: 314 286 1810
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              100.0%; Score 15; DB 17; 100.0%; Pred. No. 6.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .403 /organism="Danio rerio"
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/db_xref="taxon:7955"
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                                                  Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                         1 CCTTCTCCCCCTGTT 15
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Matches 15; Conserv
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AW139708/c
LOCUS
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BI706542/c
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/Glone="Image:271800"
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//Jab_bost="Nucl_CGAP_Sub3"
//Jab_bost="Nucl_CGAP_Sub3"
//Jab_bost="Nucl_CGAP_Larger of library derived from NCI_CGAP_Sub1 library is a subtracted library derived from B1. B1 constitutes a mixture of 21
normalized or subtracted NCI_CGAP_Larger of 21
normalized or subtracted NCI_CGAP_Larger of 21
normalized or subtracted NCI_CGAP_Larger of 21
NCI_CGAP_Rad3, NCI_CGAP_Rad1, NCI_CGAP_Col0,
NCI_CGAP_Rad3, NCI_CGAP_Rad1, NCI_CGAP_Lu24,
NCI_CGAP_Rad3, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
NCI_CGAP_Brn25, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
NCI_CGAP_Larger of 11 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:
NCI_CGAP_Rid3 pool 1 LLAM 3334-3337, 3682-3683,
3722-3725, 3776-3778 (IMAGE CloneIDS 1323912-1325831,
1471388-1472903, 14922104-1493255); NCI_CGAP_Lu5 pool 1
LLAM 3572-3372, 3373-3352, IMAGE CloneIDS 1257096-1258631,
1469064-1470983, 1475592-1476743); NCI_CGAP_PRIS Pool 1
LLAM 2457-2459, 2758-2759, 2002-2439, 2002-24109325, 121798-1222 pool 1
LLAM 2457-2459, 2758-2759, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439, 2002-2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCT-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/Amage/Amage.html The following repetitive
elements were found in this cDNA sequence: 151-216, >(GGGA
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CloneIDs 1057416-1061255, 1144584-1145351). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_LIB-NCI_CGAP_Kid3
TAG_LIB-NCI_CSAP_Kid3
TAG_RISPASSERIATIONS
TAG_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 410)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
UI-H-BII-aeb-a-03-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718605 3', mRNA sequence.
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Pred. No. 6.5e+03;
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Seq primer: M13 Forward
POLYA=No.
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Unpublished (1997)
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/clone=Inb="NCI_CGAP_Sub7"
/lab_host="NALL_CGAP_Sub7"
/lab_host="NHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)
/lab_host="Dhiop (Lif
                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs remail.nih.gov

The sequence contained an oligo-dr track that was present in the oligonoutlectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonatide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the WWW-bio.linl.gov/bbrp/image/image.html
                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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TAG_TISSUE=brain
TAG_SEQ=TTTCG"
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/clone="IMAGE:3083036"
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Best Local Similarity 100.
Matches 15; Conservative
                                                                             Tumor Gene Index
Unpublished (1997)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF514910 421 bp mRNA linear EST 07-DEC-2
UI-H-BW1-anp-a-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
IMAGE:31883036 3', mRNA sequence.
BF514910 GI:11600078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapDs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Scares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lln.gov/bbrp/image/image.html

Seq primer: M13 Forward.
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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100.0%; Pred. No. 6.5e+03;
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/db_xref="taxon:9606"
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ö Gaps .; 0 Length 421; Indels 100.0%; Score 15; DB 12; 100.0%; Pred. No. 6.5e+03; :ive 0; Mismatches 0;

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220 CCTTCTCCCCTGTT 234
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/db_xref="taxon:9606"
/dbo=lib="cr0642"
/clone_lib="cr0642"
/dev_stage="Adult"
/note="Organ: colon; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from OMESTES PCR (0.S. Letters Patent application No. 196 from Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
ысуьць25
PMO-CTO642-240401-007-CO9 CT0642 Homo sapiens CDNA, mRNA sequence.
BG961625
                                                                                                                                                                                                                           Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-CTO642-240401.007-c09&t3=2001-04-24&t4=1) Seq primer: puc 18 forward High quality sequence start: 16 High quality sequence stop: 376.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
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Populus balsamifera subsp. trichocarpa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                            BG961625.1 GI:14379796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
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QV2-NN0045-211100-494-c07 NN0045 Homo sapiens cDNA, mRNA sequence.
BQ339760.1 GI:20999826
BST
1 (bases 1 to 430)
Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H., Hiltonen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahlerao, R., Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, G. and Lundeberg, J.
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Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/sripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-211100-494-c07&t3=2000-11-21&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence start: 12
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 431)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Contact: Erlandsson R
Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Fax: 46 8 790 8287
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100.0%; Pred. No. 6.5e+03;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rikerl@biochem.kth.se.
Location/Qualifiers
                                                                                                                                                             Gene expression in Populus
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pucl8 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
75 a 138 c 108 g 110 t
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Search completed: December 11, 2002, 15;28:57

Gaps

Ouery Match 100.0%; Score 15; DB 14; Length 431; Best Local Similarity 100.0%; Pred. No. 6.5e+03; Matches 15; Conservative 0; Mismatches 0; Indels (

SUMMARIES

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. December 11, 2002, 15:30:52; Search time 1652 Seconds (without alignments) 264.251 Million cell updates/sec 4109280 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd. 2054640 segs, 14551402878 residues Total number of hits satisfying chosen parameters: Post-processing: Listing first 1000 summaries OM nucleic - nucleic search, using sw model OLIGO_NUC Gapop 60.0 , Gapext 60.0 em_sy:*
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Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 920)
Chu,T., Blumenfeld,M. and Cohen,D.
Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders
Patent: WO 0151659-A 99 19-JUL-2001;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 920)
Chu,T., Blumenfeld,M. and Cohen,D.
Biallelic markers derived from genomic regions carrying genes
involved in central nervous system disorders
Patent: WO 0151659-A 104 19-JUL-2001;
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E32679 Gene screen
BC029064 Mus muscu
AL17548 Homo sapi
AF020192 Homo sapi
AY119126 Drosophil
U62935 Aspergillus
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AK055319 Pseudomon
AX409100 Sequence
D83735 Homo sapien
AK073948 Sequence
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AK073563 Venezuela
U10564 Human CDK t
AF210627 Eremothec
AF016649 Canis fam
AC019634 Drosophil
AF338250 Sus scrof
L10342 Homo sapien
AK02564 Homo sapien
AK03557 T. thermophi
AX181862 Sequence
L13938 Sinorhizobi
AK41577 T. thermophi
AJ012716 Erwinia C
AK10550 Homo sapien
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AB005989 Homo sapi
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AX49385 Sequence
BC006460 Homo sapi
AL137684 Homo sapi
AF173159 Babesia b
M80792 Pseudomonas
              AB060971 Xenopus 1
AX429310 Sequence
AF189369 Ajellomyc
AX381046 Sequence
AX057692 Homo sapi
AJ404229 Rhodobact
AX119515 Drosophil
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Sequence 99 from Patent W00151659.
AX194629 GI:15385776
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AF338250
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Gaps

DB 6; Length 920;

100.0%; Score 15;

Query Match

Homo sapiens human.

PRI 12-JUL-2001

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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אואה שבייטיטים בייטיטים בייטיטים ואראר linear PF
Homo sapiens, clone IMAGE:3162672, mRNA, partial cds.
הברומים בייטיסים
                                                                                                                                                                                                           Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                              BC000563.1 GI:12653576
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Mammalia; Eutheria;
1 (bases 1 to 1411)
   CCTTCTCGCCCTGTT 244
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Location/Qualifiers
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The human noradrenaline transporter gene contains multiple
polyadenylation sites and two alternatively spliced C-terminal
                   Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Porzgen, P., Bonisch, H. and Bruss, M.
Molecular cloning and organization of the coding region of Muman norepinephrine transporter gene
Biochem. Biophys. Res. Commun. 215 (3), 1145-1150 (1995)
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/clone_lib="lambda FIX (Stratagene)"
129. .800
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norepinephrine transporter; SLC6A2 gene
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/usedin=X91117:SLC6A2_mRNAb
701..800
 Pred. No. 47;
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/usedin=x91117;SLC6A2_mRNAa
/usedin=x91117;SLC6A2_mRNAb
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100.0%; Score 15; DE
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Matches 15; Conservative 0; Mismatches
                  Mismatches
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/db_xref="taxon:9606"
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/cell_type="fibroblast"
                                                                                                                                                           980 bp
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/map="16q12.2"
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/gene="SLC6A2"
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Bonisch, H.
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Web site:

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Shakeshery, K.D., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,

Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,

Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,

Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,

Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 5 Row: i Column: 7
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TFSTFLLALFCITKGGIYVLTLLDTFRAGTSILFAVLMEAIGVSWFYGVDRFSNDIQO
MMGFRPGLYWRLCWKFVSPAFLLFVVVVSIINFKPLTYDDYIFPPWANWVGWGIALSS
MWGLYPIYVIXFELSTGSLWFALAYGTIPENEHHLVAQRDIRQFQLQHWLAI"
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KFDNNCYRDALLTSSINCITSFVSGFAIFSILGYMAHEHKVNIEDVATEGAGLVFILY
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Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Unknown (protein for IMAGE:3162672)"
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Pred. No. 46;
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_19"
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                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
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Matches 15; Conservative
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1 CCTTCTCGCCCTGTT 15

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/product="noradrenaline transporter"
/product="noradrenaline transporter"
/protein_id="AAA5943.1"
/db_xref="G1:189258"
/db_yref="G1:189258"

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1 (bases 1 to 1983)
Pacholczyk,T., Blakely,R.D. and Amara,S.G.
Expression oloning of a cocaine- and antidepressant-sensitive human noradrenaline transporter.
Nature 350 (6316), 350-354 (1991)
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1. .1983
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                         noradrenaline transporter.
Human, cDNA to mRNA.
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/gene="NAT1"
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                                                       Identification of a previously unknown human collagen chain, alpha 1(XV), characterized by extensive interruptions in the triple-helical region Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992) 93066196
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Myers, J.C., Kivirikko, S., Gordon, M.K., Dion, A.S. and Pihlajaniemi, T.
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Kivirikko,S., Heinamaki,P., Rehn,M., Honkanen,N., Myers,J.C. and
Pihlajaniemi,T.
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Homo sapiens (tissue library: Clontech bases 955-5167) umbilical cord (bases 1-954) cDNA to mRNA.
Homo sapiens
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HOMO Sapiens alpha-1 type XV collagen mRNA, complete cds.
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                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
/tissue_lib="g111 from Clonetech Laboratories"
/ 583 c 644 g 392 t
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/tissue_type="umbilical cord (bases 1-954)"
/tissue_lib="Clontech bases 955-5167"
1 (bases 1 to 2127)
Myers,J.C., Kivirikko,S., Gordon,M.K., Dion,A.S. and
Pihlajaniemi,T.
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1. .5161
/organism="Homo sapiens"
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1. .2127
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/note="putative"
/citation=[2]
/label=5'UTR
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/gene="COL15A1"
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Gaps

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AC020425 14621 bp DNA linear HTG 03-JAN-2000 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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Mus musculus clone RP23-117121, LOW-PASS SEQUENCE SAMPLING.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, M., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Charzoro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
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Subaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 61956)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was identified as CDM:10213135 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
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                                                                      9; Length 5161;
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/db_xref="taxon:2227"
2792 c 2769 a 4724 +
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44;
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Drosophila melanogaster
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AC101376.1 GI:17060151
HTG; HTGS_PHASE0.
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Best Local Similarity 100.
Matches 15; Conservative
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WEBECYTPGPDINEERLRATAAGEAELASMCEVEAGSGAPGELDLGAGAGGPTLSMSTE
VGPSSEDSLITTAAAATEVSLSTFEDERASWOPTDGLAPLIATMAPERRAVTSGPGDED
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KGDAGEELPGPPEPSGSPVGPTAGAERAGSGLGWGSDVGSGSGDLVGSEQLLRGPPGP
REPGLPGTPREPGGPTDVFMGPPGSGGGGWGSDVGSGGDLGCAGKGEKG
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DTEGSGSTQLLNEPKLSRPTAAIGLKGEKGDRGPKGERGAMGASIVGPPGPFGTHI
                                                                                                                                                                                                                                                 RGGVLFAITDAFQKVIYLGLRLSGVEDGHQRIILYYTEPGSHVSQEAPAFSVPVMTHR
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INTPPTPSSPFEDMELSGEPVPEGTLETTNMSIIQHSSPKQGSGEILNDTLEGVHSVD
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EQGEKGEPGAILTEDIPLERLMGKKGEPGMHGAPGPMGPKGPPGHKGEFGLPGRPGRP
GLNGLKGTKGDPGVIMQGPPGLPGPPGPPGPPGAVINIKGAIFPIPVRPHCKMPVDTA
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GDKGFKGEKGEKGDINGSFLMSGPPGLPGNPGPAGQKGETVVGPQGPPGAPGLPGPPG
FGRPGDPGPPGPPGPPAILGAAVALPGPPGPPGQPGLPGSRNLVTAFSNMDDMLQ
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PUPLSSANYERPALHAALHANIMPESCII RADPQCFKQARAAGLISTYRRAELSHLQDLS
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TITLE JOURNAL COMMENT

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jontig of 669 bp in length

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Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the record is updated, the accession number will
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of 755 bp in length
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of 679 bp in length
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contig of 675 bp in length
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682 bp in length
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11840: gap of
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10281 10969: conti
10970 11069: gap of
11070 11740: conti
11741 11840: gap of
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6290: con
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2138: co
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7853: cc
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1391: cc
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Lurect Submission

Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Si (bases 1 to 65851)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cook, A., Fitzerala, P., Fitzerald, M., Gage, D., Galagan, J., Farois, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu,G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Narden, C., Nighov, T., Mengas, V., Murphy T., Naylor, J., Meneus, L., Mihova, T., Norbu, C., Norman, C., Phunkhang, P., Pierre, W., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Seneer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Vel, R., Vo, A., Wilson, B., Wux, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
Meneus, L., Minova, T., Mutenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rettas, R., Rieback, M., Riley, R., Rise, C., Schupback, R., Scaman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stoore, J., Topham, K., Trasks, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 30, 2002 this sequence version replaced 91:21699374.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://fp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 2336: contig of 694 bp in length 137 2436: gap of 100 bp 100 bp 37 3166: contig of 634 bp in length 57 3266: gap of 100 bp 17 3987: contig of 730 bp in length 18 4087: gap of 100 bp 18 4813: contig of 726 bp in length 14913: gap of 100 bp 18 4813: contig of 726 bp in length 5651: contig of 726 bp in length 5651: contig of 726 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
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808 1542: contig of 735 bp in length

1543 1642: gap of 100 bp

1643 2336: contig of 694 bp in length
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Center clone name: 519_0_19
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2437 316
3167 3266: 9
3267 398
4088 4087: 9
4918 4913: 9
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JOURNAL
                                                                                                                                                                                                                                                                                                                        REFERENCE
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E (bases 1 to 6581)

Saliren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Burren, B., Linton, L., Bastien, V., Bloom, T., Boguslavkiy, L.,

Buckhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,

Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,

Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,

Grand-Pherre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,

Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,

Lamazares, R., Landers, T., Leboczky, J., Levine, R., Lindblad-Toh, K.,

Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 17 clone RP13-519019 map 17, LOW-PASS
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47187: contig of 677 bp in length
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3338: contig of 689 bp in length
38: gap of 100 bp
51107: contig of 669 bp in length
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672 bp in length
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of 680 bp in length
          in length
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Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP13-519019
     41784: contig of 681 bp
84: gap of 100 bp
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44096: contig
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42572: con
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Matches 15; Conserv
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KEYWORDS
SOURCE
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AC124280
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TITLE
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193 18030; 390 of 100 bp 118030; 390 of 100 bp 11805; 390 of 1180
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114: gap of 100 bp

1054: contig of 720 bp in length

1054: contig of 720 bp in length

11348: contig of 714 bp in length

148: gap of 100 bp

12160: contig of 712 bp in length
                                                                                                       100 bp
of 727 bp in length
100 bp
of 734 bp in length
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7 16272: contig of 75
3 16372: gap of 100
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....... 80669 bp DNA linear HTG 14-AUG-2002
Chlamydomonas reinhardtii clone cr-1j6, WORKING DRAFT SEQUENCE, 1
ocidered piece.
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Wu,H., Lin,S., Jia,H., Dutcher,S. and Roe,B.A.
Direct Submission
Submitted (14-AUG-2002) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales;
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This sequence will be replaced by the finished sequence as soon as it is available and
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The University Of Oklahoma
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44359: contig of 738 bp in length
4459: gap of 100 bp
45298: contig of 739 bp in length
45298: gap of 100 bp
46011: contig of 713 bp in length
                                                                                                                                                                                                    39398: contig of 721 bp in length 198: gap of 100 bp 100 bp 100 lp 100 l
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46112 46840: contig of 729 bp in length
46841 46940: gap of 100 bp
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1 (bases 1 to 80669)
Wu,H., Lin,S., Jia,H., Dutcher,S. and Roe,B.A.
Chlamydomonas reinhardtii BAC Clone cr-1j6
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25 36224: gap of 100 bp

25 36946: contig of 722 bp in

17 37046: gap of 100 bp

17 37776: contig of 730 bp in

17 37876: gap of 100 bp

17 38577: contig of 701 bp in

18 38677: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                             43: gap of 100 bp 41859: contig of 716 bp
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Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
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2 (bases 1 to 80669)
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Homo sapiens chromosome 16 clone RPll-13M21, LOW-PASS SEQUENCE
SAMPLING.
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DoE Joint Genome Institute.

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jan 26, 2000 this sequence version replaced gi:5686044.

Center: Joint Genome Institute
                                              1...80669

/organism="Chlamydomonas reinhardtii"

/db_xref="taxon:3055"

/clone="cr-1j6"

/clone_lib="cr-1j6"

/note="This is one of two clone in the same well cr-1j6"

a 25825 c 24793 g 15894 t 3 others
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                 Guery Match 100.0%; Score 15; DB 2; Length 80669; Best Local Similarity 100.0%; Pred. No. 38; Matches 15; Conservative 0; Mismatches 0; Indels 0
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* the accession number will be preserved.

* 1 80669: contig of 80669 bp in length.

Location/Qualifiers
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Mammalia; Eutheria; Primates; Cata
1. (bases 1 to 90280)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
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Web site: http://www.jgi.doe.gov
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             Ma.J., Maheshwari, M., Mapus, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Morgan, M., Moryen, N., Nedyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwunou, G., Oragunye, N., Origon, E., Nwokenkwo, S., Oguh, M., Nemore, E., Peters, L., Pickens, R., Primus, E., Pu, L. L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Riuz, S., Saverty, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stuton, A., Svatek, A., Tabor, P., Tamerisa, A., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfcod, B., Thomas, N., Tang, Y., Tansey, J., Taylor, C., Taylor, T., Telfcod, B., Thomas, N., Thomas, S., Wall, R., Washington, C., Walliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Weinstock, G. and Gibbs, R., Rous, J., Zorrilla, S., Nelson, D., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). OrdE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, T7 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15624602.
Genter: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu/
Contact: ngsc-help@bcm.tmc.edu/
Contact: ngsc-help@bcm.tmc.edu/
Contact: ngsc-help@bcm.tmc.edu/
Contact: ngsc-help@bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 115371 bases at least Q40
Consensus quality: 123148 bases at least Q30
Consensus quality: 129020 bases at least Q30
Estimated insert size: 114258; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 1.6x in Q20 bases; sum-of-contigs estimation
   Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
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------ Summary Statistics
Assembly program: Phrap; version 0.990329First call to
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COMMENT

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65025

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16075)

Chu,T., Blumenfeld,M. and Cohen,D.

Biallelic markers derived from genomic regions carrying genes

Patent: WO 0151659-A 544 19-JUL-2001;

GENSET (FR)
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contig of 1884 bp in length
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contig of 1435 bp in length
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                                                                                                                                                                    Human EST-derived
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                               MAGE-21 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                     Probe for human norepinephrine transporter gene wild type allele.
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                       AAL24145
                                                                                                                                                                                                                                                                                                                                                                        AAH28084 standard; DNA; 15 BP.
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 28-DEC-2000; 2000WO-US35491
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11-JAN-2000; 2000US-0175456.
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The present sequence represents a probe for the wild type allele of a human norepinephrine transporter gene. The specification a method for screening for susceptibility to sub-optimal norepinephrine transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful for gene therapy for modulating norepinephrine transport in a target cell and treating susceptibility to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, hypertension, heart disease, psycho stimulant abuse e.g. cocaine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single nucleotide polymorphism; SNP; biallelic marker; human; ds; central nervous system disorder; CNS; NET; norepinephrine transporter.
                                                                               Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
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/standard_name= "single nucleotide polymorphism"
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100.0%; Pred. No. 11;
ive 0; Mismatches 0;
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                                                                                                                                                   Claim 15; Page 69; 133pp; English.
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Matches 15; Conservative (
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               Blakely RD;
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                                               WPI; 2001-425681/45.
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amphetamine abuse.
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                                                      The present invention relates to biallelic markers derived from human genes involved in central nervous system (CNS) disorders. The present sequence is one such biallelic marker derived from human norepinephrine transporter (NET) gene. This marker has a single nucleotide polymorphism (SNP) and is useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes involved in central nervous system (CNS) disorders. The present sequence is one such biallelic marker derived from human noreplinephrine transporter (NET) gene. This marker has a single nucleotide polymorphism (SNP) and is useful in determining the genetic predisposition of midividuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker.
                                                                                                                                                                                                                                                                                                                                                                                                                     Single nucleotide polymorphism; SNP; biallelic marker; human; ds; central nervous system disorder; CNS; NET; norepinephrine transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to biallelic markers derived from human
biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker -
                                                                                                                                                                                                                   Gaps
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/standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                         100.0%; Score 15; DB 23; Length 920; 100.0%; Pred. No. 10;
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                                                                                                                                                                   Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;
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                                                                                                                                           least one CNS disorder related marker.
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206
                                 Claim 1; Page 248; 519pp; English.
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                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                    170 CCTTCTCGCCCTGTT 184
                                                                                                                                                                                                                                      1 CCTTCTCGCCCTGTT 15
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                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
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misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents exon 9 of the human norepinephrine transporter gene. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to conthostatic intolerance. Norepinephrine transport in a target cell and treating susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine;
                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of a exon 9 of norepinephrine transporter gene.
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                                                               23; Length 920;
                                                                                                                           Indels
Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;
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0
                                                                                                                           Mismatches
                                                        Score 15;
Pred. No.
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100.0%;
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2000US-0175456.
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/*tag= b
701..802
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                                                                                                                           Conservative
                                                                                                                                                                                                                   170 CCTTCTCGCCCTGTT 184
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                                                                                                                                                                                    1 CCTTCTCGCCCTGTT 15
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                                                            Query Match
Best Local Similarity
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us-09-750-609-9.oligo.rng

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Gaps

0;

Indels

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Length 1044;

100.0%; Score 15; DB 23; 100.0%; Pred. No. 10; Mismatches

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Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                        1 CCTTCTCGCCCTGTT 15
                                                                                                                                 97 CCTTCTCGCCCTGTT 83
                                                                                                                                                                                                                                RESULT 6
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                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                      Length 980;
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and
Sequence 980 BP; 218 A; 275 C; 246 G; 238 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #16550.
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                                                 ch 100.0%; Score 15; DB 22; Similarity 100.0%; Pred. No. 10; 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                   AAS80746 standard; cDNA; 1044 BP
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                         230 CCTTCTCGCCCTGTT 244
                                                                                                                                              1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
P-PSDB; ABG16559.
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                                                                          Sest Local Similarity
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                                                    Query Match
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Sequence 1044 BP; 229 A; 303 C; 258 G; 254 T; 0 other;

at ftp.wipo.int/pub/published_pct_sequences

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                                                                                                                                                 Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine; amphetamine abuse; ss.
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                                                                                                              Nucleotide sequence of a human norepinephrine transporter.
                                                                                                                                                                                                                                                                                                                       /product= "norepinephrine transporter"
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                                                                                                                                                                                                                                                                 Location/Qualifiers
1..1854
AAH28082 standard; DNA; 1854 BP.
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                                                                        05-SEP-2001 (first entry)
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92WO-US01376.
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                                                                                                                 15-MAR-1993 (first entry)
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                                                                                                                                                                                                                                                                                  61..1914
/*tag= a
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Best Local Similarity 100.
Matches 15; Conservative
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P-PSDB; AAR26416.
                                                                                                                                                                                                                                    Homo sapiens
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                                                                                  AAQ28118;
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                    RESULT
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                                                                                                                                                                                                                                              Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine; amphetamine abuse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
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                                                                                                                                                                                                             Nucleotide sequence of a human norepinephrine transporter.
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/product= "norepinephrine transporter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 75; Page 112-115; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                             AAH28086 standard; DNA; 1854 BP.
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11-JAN-2000; 2000US-0175456.
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                 1362 CCTTCTCGCCCTGTT 1376
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1 CCTTCTCGCCCTGTT 15
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les 15; Conserv
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Transfectants of these cells expressing the norepinepherine transporter were identified by employing an assay exploiting the fact that the norepinepherine analogue m-iodobersylguanidine (m-IBG) is accumulated intracellularly by SK-N-SH cells expressing the intact NT. The accumulated radiolabelled m-IBG allows direct autoradiographic visualisation of transporter expressing the intact NT. The accumulated radiolabelled m-IBG allows direct autoradiographic visualisation of transporter expressing the resulting plasmid pools rescreened and subdivided until a single clone was obtd. Transfected cells become capable of norepinepherine clone was obtd. Transfected cells become capable of norepinepherine adegree similar to the effect of such drugs on noradrenergic neurons. The cloned cDNA makes possible well-controlled studies of neurotransmitter transporter function in non-neuronal cells same cell. Such studies include the relative effects of various
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                                                                                                                                                                                                                                                                                                                                                                             NT; noradrenaline; neuroblastoma; neutotransmitter; antidepressant;
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                                                                                                                                                                                                                                                                               Human norepinepherine transporter protein cDNA clone.
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AAQ28118 standard; cDNA; 1983 BP.
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by CGA, by detecting the level of expression of gene(s) (GS) identified by the expression level to an expression level in an unactivated CC the expression level to an expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting CC with an agent capable of modulating GCA or an inflammation (especially cfor an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting of inflammation, an asmaple of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS, M3 is useful for modulating GCA preferably in an inflammation in a tissue; M4 is useful for creening an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic creening an inflammation (especially chronic) in a tissue, an allergic creening an inflammation (especially chronic) in a tissue, an allergic creening an inflammation (especially chronic) in a tissue, an allergic creening an inflammation (especially chronic) in a tissue, an allergic creening an inflammation (especially chronic) in a tissue, an allergic creening an inflammation (especially chronic) in a tissue, an allergic creening an inflammation (especial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                     viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatorid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; areal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                        Human cDNA differentially expressed in granulocytic cells #433.
                                                                                                                                                                                                                                                               granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     granulocyte activation; chronic inflammation; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 433; 114pp; English.
                                                    ABK83862 standard; cDNA; 5161 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beazer-Barclay Y, Weissman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2001; 2001WO-US30821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2000; 2000US-237189P.
                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-435328/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200228999-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                          14-AUG-2002
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                                                                                                     ABK83862;
RESULT 9
ABK83862/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to biallelic markers derived from human genes involved in central nervous system (CNS) disorders (see AAH88161-AAH88702). The markers have a single nucleotide polymorphism (SNP) and are useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set (genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker. The present sequence was used to illustrate the invention.
                                                                                                                                                             Gaps
sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 15; DB 23; Length 160755; 100.0%; Pred. No. 8.7; 0; Mismatches 0; Indels 0;
                                                                                                                            Length 5161;
                                                                                                                                                                                                                                                                                                                                                                                                                            Single nucleotide polymorphism; SNP; biallelic marker; human;
                                                                                          Sequence 5161 BP; 1254 A; 1420 C; 1363 G; 1124 T; 0 other;
                                                                                                                                                          0; Indels
                                                                                                                      100.0%; Score 15; DB 24;
100.0%; Pred. No. 9.6;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           central nervous system disorder; CNS; ds.
                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 476-519; 519pp; English.
                                                                                                                                                                                                                                                                                               AAH88704 standard; DNA; 160755 BP.
                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                             Human DNA sequence SEQ ID 544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2001; 2001WO-IB00116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JAN-2000; 2000US-0175854.
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 63345 CCTTCTCGCCCTGTT 63359
                                                                                                                                                       15; Conservative
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                                                                                                                                                                                      1 CCTTCTCGCCCTGTT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blumenfeld M,
                                                                                                                                                                                                        2673 CCTTCTCGCCCTGTT
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                                                                                                                                   Best Local Similarity
Matches 15; Conserv
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                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                   RESULT 10
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RESULT 11

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 336 BP; 61 A; 101 C; 109 G; 64 T; 1 other;
                                                                                 Human ORFX polynucleotide sequence SEQ ID NO:4669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID 4669; 1037pp; English.
          ABN18096 standard; cDNA; 336 BP.
                                                                                                                                                                                          myasthenia gravis; gene; ss.
                                                                                                                                                                                                                                                                                                               30-MAY-2000; 2000US-206132P. 29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                       29-MAY-2001; 2001WO-US10836.
                                                         24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                           Leach MD;
                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ABP02344.
                                                                                                                                                                                                                                         WO200192523-A2
                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA,
                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                               06-DEC-2001.
                                ABN18096;
ABN18096
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27552 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder. ORFX polynucleotide syndrome associated with ORFX-associated disorder. ORFX polynucleotide syndrome associated with ORFX-associated disorder. ORFX polynucleotide creatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious attritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.3%; Scor.
100.0%; Pred. No. 4c,
0; Mismatches
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0

Gaps

; 0

0; Indels

Matches 14; Conservative

Query Match Best Local Similarity

Score 14; DB 24; Length 336; Pred. No. 40;

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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (AB054131-AB05605), and also encompasses polypeptides 90% identical and polypucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens, and thodies against human ovarian antigens, and the use complexity prognosing or preventing various ovary and/or breast-related of ovarian antigen polypucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related clasorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertility, disorders (e.g., mastitis, oophoritis and cashock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and immunodeficiencies, auctimunue ophoritis, systemic lasorders, candisorders (e.g., anaemia), cardiovascular disorders condurinary system disorders, neurological disorders, gastrointestinal disorders condurinary system disorders, ovarian antigen polypeptides and curinary also expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the
                                                                                                                                                                                                                                                                                                                                                                                       syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                                                           ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndriptock; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid molecules encoding novel ovarian polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                           Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                                                            Human ovarian antigen HVVAW26 cDNA, SEQ ID NO:2083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 2083; 2922pp; English.
                                                                                                                                                        ABQ56203 standard; cDNA; 655 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                                                                               22-AUG-2002 (first entry)
2 CTTCTCGCCCTGTT 15
                       82 CTTCTCGCCCTGTT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200200677-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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Length 708;

0 other;

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Sequence 708 BP; 152 A; 212 C; 196 G; 148 T;
                                    Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001
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                                                                                                                                                                                                              ABL11823;
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Matches
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                                                                                                                                                                       ABL11823,
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                         ó
                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
         polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                       Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID NO: 534; 246pp + Sequence Listing; English.
                                                                                                                                           93.3%; Score 14; DB 24; Length 655; 100.0%; Pred. No. 39; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ochiai K,
identification of individuals and in forensic analysis,
                                                                                                                    Sequence 655 BP; 182 A; 168 C; 177 G; 116 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                              glutamicum coding sequence fragment SEQ ID NO: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                      499/c
AAH65499 standard; DNA; 708
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                                                                                                                                                                                                                                                                                                                                                                                                                     organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                   556 CTTCTCGCCCTGTT 543
                                                                                                                                                                                                   2 CTTCTCGCCCTGTT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-376931/40
                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakagawa S,
Tateishi N,
                                                     invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention siscloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster expressed polynucleotide SEQ ID NO 29951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
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ABL11823 standard; cDNA; 2036 BP.
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The 20.5 game, also referred to as Tea, identifies transcripts found in only a limited number of tissues. Tea transcripts are induced in splenocytes activated with the T cell mitogen ConA. Unlike other known genes expressed in activated T cells, the Tea gene appears to encode a protein which traverses the membrane multiple times, whereas the large number of known integral membrane protein which are induced in T cell activation are single membrane spanning proteins. See also AAQ14530-34.
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4 US-09-073-297-1 4 US-09-296-284-52 5 PCT-US1-06532-1 1 US-08-087-72A-4 1 US-08-979-608A-12 1 US-08-265-087-3 1 US-08-265-087-3 1 US-08-92-10-982-1 4 US-09-10-982-1 1 US-08-118-1274-43 1 US-08-149-043-43 1 US-08-449-043-43 1 US-08-449-043-43 1 US-08-456-265A-43 1 US-08-456-265A-43 1 US-08-456-265A-43 1 US-08-456-265A-43 1 US-08-456-265A-43	2 US-08-457-364-43 2 US-08-456-262-43 2 US-08-456-262-43 2 US-08-456-243-43 2 US-08-456-243-43 2 US-08-971-743 4 US-09-350-600-43 4 US-09-350-600-43 4 US-08-814-764-11 8 US-08-814-764-11 8 US-08-91-114-17 1 US-08-097-8618-11 1 US-08-979-668A-13 1 US-08-979-668A-13 1 US-08-492-985-1 1 US-08-491-772-7 1 US-09-492-988-1	US-09-687-594-17 US-09-149-476-139 US-08-392-338A-18 US-09-166-750-18 US-09-166-094-18 US-09-172-019-18 US-09-172-019-18 US-09-172-019-18 US-09-172-019-18 US-09-178-11-3 US-08-354-85-11 US-09-492-985-11 US-09-298-118-6 US-09-298-718-6 US-09-298-718-6 US-09-298-718-6 US-09-298-718-6 US-09-298-718-6 US-08-318-837-6 US-08-318-837-6 US-08-318-837-6 US-08-318-837-6 US-08-318-837-6 US-08-318-837-6 US-08-318-837-6	2 US-09-315-850-3 2 US-09-315-850-3 2 US-08-850-910A-17 4 US-08-850-910A-38 2 US-08-815-667-10 2 US-08-1716-942-24 2 US-09-130-337A-24 2 US-09-329-418-2 3 US-09-329-418-2 4 US-09-511-11-1 1 US-07-669-171-1 1 US-07-669-171-1 1 US-07-669-171-3 4 US-09-659-171-3 1 US-08-689-174-2 3 US-08-689-174-3 4 US-08-689-174-2 3 US-08-689-174-3 4 US-08-689-174-3 4 US-08-689-174-2 3 US-08-08-376-2 4 US-08-08-376-2 4 US-09-620-412C-188
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1 US-08-462-195-1 2 US-08-16-883-1 3 US-09-127-829-1 4 US-09-127-829-1 1 US-09-500-651-1 1 US-08-813-567-1 1 US-08-813-567-1 1 US-08-813-567-1 1 US-08-325-92A-97 1 US-08-945-515-1 1 US-09-256-877-283 1 US-09-221-0178-203 1 US-09-221-0178-203 1 US-09-287-375-13 1 US-09-287-375-13 1 US-09-287-406-13 1 US-09-287-406-13 1 US-09-287-406-13 1 US-09-287-406-13 1 US-09-296-284-57	US-09-296-284-56 US-09-296-284-56 US-09-09-2451-9 US-09-09-322-9 US-09-09-372-1 US-08-324-977-9 US-08-384-616-9 US-09-296-284-55	US-09-239-284-54 US-09-232-200-54 US-09-232-197-54 US-08-862-82A-56 US-09-221-017B-56 US-09-221-017B-56 US-09-221-017B-56 US-08-26-429A-4 PCT-US95-09069-4 US-09-232-191-18 US-09-232-191-18 US-09-232-191-18 US-09-232-191-18 US-09-232-191-18 US-09-232-191-18 US-09-232-191-18 US-08-146-010A-4 US-08-146-010A-4 US-08-148-9 US-08-148-9 US-08-148-9	US-08-860-882A-71 US-09-296-284-53 US-09-011-769A-55 US-09-011-769A-55 US-09-023-471A-37 US-09-025-691-2 US-09-029-755C-6 US-09-029-755C-6 US-09-029-755C-6 US-09-056-105-24 US-09-056-105-24 US-09-851-520-3 US-08-851-520-3 US-08-851-520-3 US-08-038-948-1 US-08-038-952-4 US-08-038-948-1 US-08-483-952-4 US-08-483-952-4 US-08-483-952-4 US-08-483-33-36 US-09-283-471A-36
1037 1 1037 2 1037 3 1056 1 1056 1 1065 1 1065 1 1077 4 1077 4 1081 2 1081 4 1081 4 1107 4	1134 11466 4 4 11166 4 4 1 11161 1 1167 1 1167 2 1167 2 1167 4 4 4 1 1169 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	12.248 4 4 1 1 1 1 1 1 2 2 4 8 4 4 1 1 1 2 4 8 8 4 4 1 1 2 2 6 9 1 1 2 2 9 8 4 4 1 1 2 2 9 8 4 4 1 1 2 2 9 9 1 1 2 2 9 9 1 1 2 2 9 9 1 1 2 2 9 9 1 1 2 2 9 9 1 1 2 2 9 9 1 1 2 2 9 9 9 1 1 2 2 9 9 9 9	2844 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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4 US-09-221-017B-234 US-08-087-772A-1 US-08-087-772A-1 US-08-085-7414-1 US-08-08-045-176A-1 US-09-431-470-3 US-08-295-060-3 US-08-291-22 US-08-291-22 US-08-291-22 US-08-285-08414-1 US-09-257-089-1 US-09-257-089-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-08-285-08414-1 US-09-285-08414-1	4 US-09-222-201-74 1 US-07-288-790B-5 4 US-09-605-785-469 4 US-09-352-616A-469 4 US-09-352-616A-469 4 US-09-352-616A-469 4 US-09-251-225 1 US-08-961-527-265 1 US-08-961-527-265 1 US-08-961-527-3 1 US-08-676-974-5 2 US-09-088-487-5 2 US-09-233-785-2
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US-09-434-288-1 US-08-855-518-2 US-08-855-518-2 US-08-970A-22 US-08-970A-22 US-08-929-68A-11 US-08-929-22 US-08-929-22 US-08-929-22 US-09-92-22 US-09-92-22 US-09-92-22 US-08-829-22 US-08-829-22 US-08-829-22 US-08-829-22 US-08-92-22 US-08-92-23 US-08-92-22 US-08-92-22 US-08-92-22 US-08-92-22 US-08-92-23 US-08-92-93 US-09-92-93	US-09-363-970-34 US-08-532-547-6 US-08-532-547-8 US-09-019-809-6 US-09-011-809-8 US-09-471-177-6 US-09-54-129-7 US-09-54-129-7 US-08-933-7500-95 US-08-933-7500-95 US-08-999-774A-9
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Gaps

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APPLICANT: MacLeod Dr., Carol L.
TITLE OF INVENTION: No. 5440017el T-cell Lymphoma cDNA Clones
NUMBER OF SECUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Patent Department, Fulbright & Jaworski
STREET: 101301 McKinney, Suite 5100
CITY: Houston
                                                                                                                                                                                 Length 2397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITT: HOUSELOWS

STATE: TEXAS

COUNTRY: USA

ZIP: 77010-3095

COMPTTER PADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,999
FILING DATE: 19930111
CLASSIFICATION NUMBER: US/08/322
FILING DATE: 19930111
CLASSIFICATION NUMBER: US/08/322
FILING DATE: 11-APR-11991
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Benjamin A.
REGISTRATION NUMBER: U-5232-DIV
TELEFRONG (713) 651-5587
TELECOMMUNICATION INFORMATION:
TELEFRONE: (713) 651-5246
TELEFAX: UNCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: Innear
MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
ORGANISM: MOUSE
CTPATIN: AKRI Jackson
                                                                                                                                                                                 93.3%; Score 14; DB 1;
100.0%; Pred. No. 3.5;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.3%; Score 14; DB 1; 100.0%; Pred. No. 3.5;
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INDIVIDUAL ISOLATE: SL12 cell line
TISSUE TYPE: Lymphoma
CELL TYPE: T-cell
CELL LINE: SL12.3 and SL12.4
                        SL12 cell line
; STRAIN: AKRI Jackson
; INDIVIDDAL ISCLATE: SL12 cell l
; TISSUE TYPE: Lymphoma
; CELL TYPE: T-cell
; CELL LINE: SL12.3 and SL12.4
; LLMBDIATE SOURCE:
; CLONE: 20.5
US-07-686-322A-5
                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08002999; Sequence 10, Application US/08002999; Patent No. 5440017; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     1379 CTTCTCGCCCTGTT 1392
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Best Local Similarity
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Best Local Similarity
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CLONE: 20.5
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Sequence 2, Appli
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Sequence 11, Appl
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                        Sequence 1
Sequence 1
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Sequence 5, Application US/07686322A
Patent No. 5312733
GENERAL INFORMATION:
APPLICANT: MacLeod Dr., Carol L.
TITLE OF INVENTION: No. 5312733el T-cell Lymphoma cDNA Clones
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Patent Department, Fulbright & Jaworski
STREET: 1301 McKinney, Suit 5100
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNATE: 14285
COUNTRY: USA
ZIP: 77010-3095
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/686,322A
FILING DATE: 19910411
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/509684
FILING DATE: 13-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       US-09-352-616A-470
                                                                                                                                                              US-09-605-785-470
US-09-439-313-470
                                                                                                                       5248599-1
US-09-624-693A-12
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US-09-513-007-1
US-08-542-363-3
US-09-100-089-3
US-09-670-827-3
US-08-981-392-1
                                       US-08-608-241-1
US-08-922-182-1
US-08-919-953-1
US-09-192-983-1
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US-09-073-663-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Launer, Charlene A.
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: D-5232-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-3634
TELEX: Western Union 762829
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                             5168051-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                         2408
2408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Texas
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US-07-686-322A-5
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USA
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US-09-400-208B-22/c
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COUNTRY: U
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APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
  Gaps
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  Indels
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  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,990A
FILLING DATE: 29-UN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05569
FILLING DATE: 11-UN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/899,075
FILLING DATE: 11-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/899,075
FILLING DATE: 11-UN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILLING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               IE: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                     Sequence 5, Application US/08132990A Patent No. 5834589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/627,950
FILING DATE: 14-DEC-1990
ATTORNEY AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
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0
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2397 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66441 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 14; Conservative
                                                                        Db 1379 CTTCTCGCCCTGTT 1392
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STRANDEDNESS: single
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                                      2 CTTCTCGCCCTGTT 15
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                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      New York
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                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                    US-08-132-990A-5
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                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                    STREET:
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Matches
                                                                                                                                RESULT 3
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SERVING NO. 6271011

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lee, Margie
APPLICANT: Sanchez, Susan
APPLICANT: Henk, Adam
TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
TITLE OF INVENTION: Compositions and Diagnostic Methods
TITLE OF INVENTION: Compositions and Diagnostic Methods
FILE REFERENCE: 77-96B
CURRENT APPLICATION NUMBER: US/09/400, 208B
CURRENT FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 60/028,876
PRIOR APPLICATION NUMBER: US 60/028,876
PRIOR FILING DATE: 1996-10-16
PRIOR FILING DATE: 1996-10-16
PRIOR FILING DATE: US 60/028,482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                           APPLICANT: MENUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.3%; Score 14; DB 5; Length 2397; 100.0%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09382
FILING DATE: 19921213
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MERUELO=1
                                                                                                                                                                                                                                                                                                                                   ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 22, Application US/09400208B
; Patent No. 6271011
Sequence 5, Application PC/TUS9209382 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION UNDBER: 33,949
REFERENCE/DOCKET NUMBER: MERUE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-5197
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1996-10-15
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Matches 14; Conservative
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; LOCATION: 410..1768
PCT-US92-09382-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
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Gaps

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Sequence 6, Application US/09491522
Sequence 6, Application US/09491522
Patent No. 642898
GENERAL INFORMATION:
APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Lee, Margie
APPLICANT: Sanchez, Susan
APPLICANT: Henk, Adam
TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
TITLE OF INVENTION: Compositions and Diagnostic Methods
FILE REFERENCE: 77-968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2001;
                                                                                                                                                                                                                           86.7%; Score 13; DB 4; Length 497; 100.0%; Pred. No. 15; 0; Indels Live 0; Mismatches 0; Indels
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; Pred. No. 14;
0; Mismatches
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PRIOR FILING DATE: 1997-10-15
PRIOR FILICATION NUMBER: US 60/028,876
PRIOR FILING DATE: 1996-10-16
PRIOR FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/400,208B
CURRENT FILING DATE: 1999-09-21
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09400208B Patent No. 6271011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Pasteurella multocida
                                                                                               TYPE: DNA ORGANISM: Pasteurella multocida
PatentIn Ver. 2.0
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                              Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
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; NAME/KEY: mat_peptide
; LOCATION: (251)..(1486)
US-09-400-208B-4
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CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-400-208B-4/c
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                                                                                                                                                                 US-09-400-208B-24
                           SEQ ID NO 24
LENGTH: 497
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SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lee, Margie
APPLICANT: Sanchez, Susan
APPLICANT: Sanchez, Susan
APPLICANT: Sanchez, Susan
APPLICANT: Henk, Adam
TITLE OF INVENTION: Compositions and Diagnostic Methods
TITLE OF INVENTION: Compositions and Diagnostic Methods
FILE REFERENCE: 77-96B
CURRENT APPLICATION NUMBER: US/09/400,20BB
CURRENT FILING DATE: 1999-09-21
PRIOR FILING DATE: 1999-09-21
PRIOR FILING DATE: 1996-10-15
PRIOR FILING DATE: 1996-10-16
PRIOR FILING DATE: 1996-10-16
PRIOR FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN Ver. 2.0
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Sequence 24, Application US/09400208B
Patent No. 6271011
SERENBAL INFORMATION:
APPLICANT: Lee, Margie
APPLICANT: Sanchez, Susan
APPLICANT: Henk, Adam
TITLE OF INVENTION: Compositions and Diagnostic Methods
FILE REFERENCE: 77-96B
CURRENT APPLICATION NUMBER: US/09/400, 208B
CURRENT FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 60/028, 876
PRIOR APPLICATION NUMBER: US 60/028, 876
PRIOR FILING DATE: 1996-10-16
PRIOR APPLICATION NUMBER: US 60/028, 876
PRIOR APPLICATION NUMBER: US 60/028, 876
PRIOR APPLICATION NUMBER: US 60/028, 876
PRIOR APPLICATION NUMBER: US 60/028, 886
PRIOR FILING DATE: 1996-10-16
PRIOR APPLICATION NUMBER: US 60/028, 887
PRIOR FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/09400208B Patent No. 6271011
                                                                                                                              TYPE: DNA ORGANISM: Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Pasteurella multocida US-09-400-208B-23
                                  Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 13; Conservative
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NUMBER OF SEQ ID NOS:
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Best Local Similarity
Matches 13; Conserv
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APPLICANT: Lee, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-400-208B-23/c
   NUMBEL.
SOFTWARE: Pate
SEQ ID NO 22
                                                                                                                                                                                               US-09-400-208B-22
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LENGTH: 491
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Gaps

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DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
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MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: WordPerfect 8 for Windows
                                                                                                                                                                                                                                                           Score 13; DB 4; Length 2450; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MORENO VALLE, Migeul Angel
SALTO MALDONADO, Francisco
DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (C) REF./DOCKET NO.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BARREDO FUENTE, Jose Luis
RODRIGUEZ SAIZ, Marta
COLLADOS DE LA VIEJA, Alfonso J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,337A
FILING DATE: 14-May-1999
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MASS, Clifford J. REGISTRATION NUMBER: 30,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: LADAS & PARRY STREET: 26 WEST 61 STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4, Application US/09171337A
; Patent No. 6300095
; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-555
TELEX: 660-493-556
TELEX: 66141 PENNE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENTH: 2450 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleotides
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                           86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                  511 CCTTCTCGCCCTG 499
                                                                                                                                                                                                                                                                                                                                          1 CCTTCTCGCCCTG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
                                                                                                                                                                                              ; TOPOLOGY: linear
US-09-491-522-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
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US-09-171-337A-4/C
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APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin V.
ATITLE OF INVENTION: RECOMBENANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.7%; Score 13; DB 4; Length 2023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                  OPERATING STEPR: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: Windows SPSTWARE: PSSYSEQ for Windows Version 2.0b SOFTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0060-999
                                                                                                                                                                                                                                                                                                                                                              8389-0900-688
                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,605
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 2023 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09491522
Patent No. 6428998
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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    COUNTRIED COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 CCTTCTCGCCCTG 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-09-491-522-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
Les 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1155 Av
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-491-522-2/c
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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U-011948-3

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/label= actin_gene
/note= "Nucleotide sequence of region B in Figure
60. Sequence corresponds to Figure 62."
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patent No. 6090607

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: ENHANCED EXPRESSION OF
TITLE OF INVENTION: PROTEOLYTIC ENZYMES IN KOJI MOLDS
NUMBER OF SEQUENCES: 17
COMPUTER READABLE Floopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/254,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(1294..1300, 1428..1458, 1631..1686, 1797
..1827, 1918..2689, 2757..2984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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14;
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                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FBATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 4657 base pairs
               LENGTH: 3748 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         1294..1300
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1428..1458
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1797..1827
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2757..2984
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                                                                                                                                                      NAME/KEY: - ...3748
LOCATION: 1...3748
COTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: FEATURE: NAME/KEY: exon LOCATION: 1294..1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCTTCTCGCCCTG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
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US-09-254-325-1
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zushi, Mitichitaka
APPLICANT: Gomi, Komakazu
APPLICANT: Gomi, Komakazu
APPLICANT: Susuki, Koji
APPLICANT: Suzuki, Koji
APPLICANT: Matsuda, Akio
TITLE OF INVENTION: A Polypeptide Capable of Interacting
TITLE OF INVENTION: with Thrombin
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.7%; Score 13; DB 4; Best Local Similarity 100.0%; Pred. No. 14; Matches 13; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 N. Washington St. CITY: Falls Church
         ORGANISM: Penicillum chrysogenum IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                         LOCATION: 2183...2249
CHER INFORMATION: act gene
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-171-337A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/261,206
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30330 REFERENCE/DCKET NUMBER: 216-275P TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-261-206A-76/c
; Sequence 76, Application US/08261206A
; Datent No. 5574007
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       1321...1410
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794...920
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INFORMATION FOR SEQ ID NO: 76:
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                                                  CLONE: <Unknown>
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ORIGINAL SOURCE:
                                                                                      NAME/KEY:
LOCATION:
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Indels

Pred. No. 14; Mismatches

13

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Best Local Similarity 100.0%; P
Matches 13; Conservative 0;
                                                                      511 CCTTCTCGCCCTG 499
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US-08-319-387-1/C
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APPLICANT: Colige, Alain
APPLICANT: Laplace, Charles M.
APPLICANT: Laplace, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                    /label= TRUNCATED-AREA
/note = "AREA IS TRUNCATED IMMEDIATELY
DOWNSTREAM THE SEQUENCE ENCODING
A DNA BINDING DOMAIN"
                                                                                                                                                                                                                                                                                           Length 4657;
                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                           DB 3;
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0060-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                           Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                             86.7%; SCUL.
100.0%; Pre
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-491-522-1/c
; Sequence 1, Application US/09491522
; Patent No. 6428998
                                                                                                                                                 misc_feature
1189..3480
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                                                                                                   exon
1704..3846
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 6692 base pai
TYPE: nucleic acid
STRANDEDNESS: single
exon
1189..1604
                                                                 1605..1703
                                                                                                                                                                                                                                                                                                                                                                               4557 CTTCTCGCCCTGT 4569
                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-09-254-325-1
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Best Local Similarity
Matches 13; Conserv
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LOCATION:
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LOCATION:
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FEATURE:
               LOCATION:
NAME/KEY:
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DB 4;

86.7%; Score 13;

Query Match

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Sequence 1, Application US/08319387

Sequence 1, Application US/08319387

GENERAL INFORMATION:
APPLICANT: Shields, Malcolm S.
APPLICANT: Arancesconi, Stephen C.
TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Dichloroethylenes and Aromatic Pollutants NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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red. No. 14;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/319,387
                                                                                                                                                                                                                E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 11, 2002, 19:01:33 Job time: 70.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/167,457
FILING DATE: 15-DEC-1993
CLASSIFICATION AAPA:
APPLICATION WARP:
APPLICATION NUMBER: US 07/694,718
FILING DATE: 02-MAY-1991
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UWI
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TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 904-3/2000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRNGTH: 9785 base pairs
                                                                                                                                                                                                                                                                            STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                       STREET: 2421 N.W. CITY: Gainesville
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Appli Appli

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Sequence 5, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 240, Appl
Sequence 225, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 16581, Appl
Sequence 16581, Appl
Sequence 16581, Appl
Sequence 149, Appl
Sequence 149, Appl
Sequence 149, Appl
Sequence 1270, Appl
Sequ
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               Sequence Sequence Sequence Sequence
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0 US-09-917-800A-1074
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US-09-966-546-25 US-09-966-545-25 US-09-833-381-1175 US-09-887-576-802 US-09-815-242-5968	US-09-815-242-9836 US-09-934-778-1	US-09-815-242-9304 US-09-935-390A-11	JS-09-924-400-9 US-09-810-936-9	US-09-429-755-9	US-US-143-143 US-09-895-913A-55	US-09-815-242-7383	US-09-831-194-3 US-09-815-242-7518	US-09-822-830A-414	US-U9-961-52/A-18	US-09-729-835-26	US-09-815-242-4132	US-09-924-256A-87	US-09-143-12/-9 US-09-925-301-127	US-10-044-090-236	US-09-974-300-2319	US-09-974-300-8308	US-09-974-300-909	US-U9-764-8/7-2363	US-09-765-205-17	US-09-974-300-38	US-09-925-301-538	US-09-764-864-551	US-U9-80T-368-79 IS-00-071-536-20	US-09-9/II-336-29 US-09-815-242-7780	US-09-974-300-1172	JS-09-938-842A-1752	US-09-815-242-4153	US-10-US2-545-1 IIS-09-887-054-1	US-09-815-242-7186	US-09-943-671-18	US-10-044-090-177	US-10-027-559-11	JS-09-938-842A-2090	US-09-057-951-3	US-10-105-150-3	US-09-748-033-2 US-09-867-550-1319	US-09-815-242-9140	US-09-887-576-783	US-09-974-300-6231	15-09-8/4-503-5	US-10-006-867-155	US-09-864-761-16987	US-09-954-456-1141	US-09-829-482-1	US-U9-809-545A-1	US-09-141-869-212 US-09-790-264-35	115-109-795-693-12	US-09-801-368-129	US-09-756-283A-21	US-09-741-669-192	US-09-815-242-6624	US-09-962-055-12	US-10-023-529-12	US-10-023-523-12
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Sequence 1166, Ap Sequence 45, App Sequence 45, Appl Sequence 14, Appl Sequence 11, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl Sequence 107, Appl Sequence 110, Appl Sequen
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APPLICANT: Boehringer Ingelheim Pharma KG
TITLE OF INVENTION: Method for identifying substances which positively
TITLE OF INVENTION: influence influenctory conditions of chronic
TITLE OF INVENTION: influence influe
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0.8-09-179-307-9
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US-09-764-878-258/c
Sequence 258, Application US/09764878
; Patent No. US20020090615Al
; GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
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Sequence 1, Application US/09430029;
Patent No. US20020168738A1
Sequence 1, Patent No. US20020168738A1
Sequence 1, Sequence 1
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBNCE: PC008
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198
SOFTWARE: Patentin Ver. 2.0
             TITLE OF INVENTION: Uncleic Acids, Proteins, and Antibodies FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 428
SOFTWARE: Patentin Ver. 2.0
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; Patent No. US20020094953A1
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ORGANISM: Burkholderia cepacia
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Best Local Similarity 100.
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US-09-764-878-258
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APPLICANT: Rosen et al
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US-09-764-860-937/c
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LENGTH: 4558
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Patent No. US20020048763A1
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                                                                             31 CCTTCTCGCCCT 42
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APPLICANT: Eisen, Herman N.
APPLICANT: Eisen, Herman N.
APPLICANT: Eisen, Herman N.
APPLICANT: Eisen, Herman N.
TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
TITLE OF INVENTION: CD4+T Cell-Independent
FILE REFERENCE: 0399.2006-003
CURRENT APPLICATION NUMBER: US/09/761,534A
CURRENT FILING DATE: 2001-01-16
PRIOR PRILING DATE: 2000-12-14
PRIOR FILING DATE: 3000-12-14
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Pred. No. 9.9;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: PCR Primer oQH011
US-09-761-534A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09761534A Patent No. US20020146426Al GENERAL INFORMATION:
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APPLICANT: Richmond, Joan F.L.
APPLICANT: Cho, Bryan K.
APPLICANT: Palliser, Deborah
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                               OCHER INFORMATION: tomn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . OTHER INFORMATION: tomQ US-09-430-029-1
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                                                                                                                                                                                                                                                      LOCATION: (1495)..(1761)
OTHER INFORMATION: tomM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (3810)..(4871)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (3428)..(3781)
OTHER INFORMATION: tomO
                                               LOCATION: (234)..(443)
OTHER INFORMATION: LOMK
                                                                                                                       NAME/KEY: CDS
LOCATION: (463)..(1455)
OTHER INFORMATION: tomL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (3810)..(4871)
OTHER INFORMATION: LOMP
FEATURE:
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Best Local Similarity
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                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
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LOCATION: (342)
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LOCATION: (48)
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LENGTH: 49
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N: EXPRESSED IN HELA, SIGNAL = 2.4

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

N: EXPRESSED IN BRAIN, SIGNAL = 2.3

N: EXPRESSED IN HEART, SIGNAL = 1.8

N: EXPRESSED IN PLACENTA, SIGNAL = 1.5

N: EXPRESSED IN PLACENTA, SIGNAL = 1.4

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.1

N: EXPRESSED IN HBL100, SIGNAL = 1.8
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SEQ ID NO 17150
LENGTH: 152
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Sequence 5128, Application US/09983965
Patent No. US20020137160A1
GENERAL INFORMATION:
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF LINGERICE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1998-12-17
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                                                  80.0%; Score 12; DB 10; Length 235; 100.0%; Pred. No. 46;
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APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID MOSS: 10912
SOFTWARE: FASTSEQ for Windows Version 4.0
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100.0%; Pred. No. 45;
iive 0; Mismatches 0
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                                                                                           0; Mismatches
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2.09-867-701-5624
; Sequence 5624, Application US/09867701
; Patent No. US20020132237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.0
Best Local Similarity 100.
Matches 12; Conservative
                                                                                             Conservative
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SEQ ID NO 5128
LENGTH: 356
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216 CTTCTCGCCCTG 205
                                                                                                                                       2 CTTCTCGCCCTG 13
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                                                  Query Match
Best Local Similarity
Matches 12; Conserv
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         US-09-923-876-97
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APPLICANT: Lalgudi, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: 05/09/923,876
CURRENT PAPPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SEQ ID NO 97
LENGTH: 235
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700142552H1
                                                                                                                                80.0%; Score 12; DB 10; Length 152;
100.0%; Pred. No. 46;
tive 0; Mismatches 0; Indels
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46;
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APPLICANT: Berka, Randy M.
APPLICANT: Dausen, 1D Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-02
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR PLICATION NUMBER: 60/279,526
PRIOR PLING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-13-05
PRIOR FILING DATE: 2000-13-05
PRIOR FILING DATE: 2000-13-05
NUMBER OF SEQ ID NOS: 8481
SOFTMARE: FASISEQ for Windows Version 4.0
  EXPRESSED IN FETAL LIVER, SIGNAL = 1.4 RXPRESSED IN LUNG, SIGNAL = 2 TH HIT: ALIG3303.2, EVALUE 1.00e-80 SWISSPROT HIT: 060241, EYALUE 4.00e+00
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100.0%; Pred. No. 46;
tive 0; Mismatches
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                                                                                                                                                                              12; Conservative
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US-09-974-300-7193
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Best Local Similarity 100.
Matches 12; Conservative
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56 CTTCTCGCCCTG 67
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CTHER INFORMATION: E
COTHER INFORMATION: E
COTHER INFORMATION: N
CTHER INFORMATION: S
US-09-864-761-17150
                                                                                                                                  Query Match
Best Local Similarity
Matches 12; Conserv
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US-09-974-300-7193/c
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LENGTH: 173
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Sequence 880, Application US/09954531

Sequence 880, Application US/09954531

Sequence 880, Naphlication US/09954531

Sequence 880, Naphlication US/09954531

Sequence 880, Naphlication US/09954531

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using FILE FOR FUNCHION: Gene Sets

FILE EPERBACE: 689290-77

CURRENT APPLICATION NUMBER: US/06/233, 133

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234, 509

PRIOR PLING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 1392

SOFTWARE: PatentIn Version 3.0.

LENGTH: 414
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US-09-864-761-337

Sequence 337, Application US/09864761

SERBEAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL.

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-x-1

CURRENT APPLICATION NUMBER: US 60/180, 312

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207, 456

PRIOR APPLICATION NUMBER: US 60/207, 456

PRIOR PRILING DATE: 2000-05-26

PRIOR PRILING DATE: 2000-05-26

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PRIOR FILING DATE: 2000-05-26
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                                                   DB 10; Length 396;
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. 45;
                                                                                                                                                0; Mismatches
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                                                   80.0%; Score 12; 100.0%; Pred. No.
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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100.0%;
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Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                  283 CTTCTCGCCCTG 272
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US-09-954-531-880/c
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                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFUREATION:

APPLICANT: Rank David R.

APPLICANT: Rank David R.

APPLICANT: Rank David R.

APPLICANT: Hancal, David R.

APPLICANT: Hancal, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aconica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR PLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-00-04

PRIOR FILING DATE: 2000-00-04

PRIOR FILING DATE: 2000-00-07

PRIOR PLICATION NUMBER: US 60/235,366

PRIOR FILING DATE: 2000-00-07

PRIOR PLICATION NUMBER: DET/US01/00666

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2001-01-30

PRIOR PLICATION NUMBER: PCT/US01/00664

PRIOR PLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR PLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR PLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLICATION NUMBER: PCT/US01/00664
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N: EXPRESSED IN HERRT, SIGNAL = 2.9

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3

N: EXPRESSED IN BT474, SIGNAL = 1.4

N: EXPRESSED IN BT474, SIGNAL = 2.7

N: EXPRESSED IN HELA, SIGNAL = 2.7

N: EXPRESSED IN HELA, SIGNAL = 3.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

N: EXPRESSED IN LOUG, SIGNAL = 1.2
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/714,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                    Sequence 3392, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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19 TCTCGCCCTGTT 30
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OTHER INFORMATION: EX
OTHER INFORM
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GENERAL INCOMMATION:

APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR PELICATION NUMBER: US/60/234,009
PRIOR PELICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR PELICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR PELICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR PELICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
PRIOR PELICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
PRIOR PELICATION NUMBER: US/60/234,567
PRIOR PELING DATE: 2000-09-22
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               COMPUTER: Diskette - 3.5 inch, 1.44 Mb COMPUTER: IBM compatible PC OPERATING SYSTEM: Windows 95 SOFTWARE: Word 97 (DOS text format) APPLICATION DATA:
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APPLICATION NUMBER: 09/018,584
FILING DATE: 04-Feb-1998
ATTORNEY/AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 16026.9180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 257-3501
TELEPHONE: (608) 257-3501
TELEPHONE: (608) 257-2275
INFORMATION FOR SEQ. ID NO: 17
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/784,423
FILING DATE: 15-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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CLONE: G158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 447 bp
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0
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LOCATION: (1)...(461)
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US-09-954-531-813/c
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REPEAT DNA MARKERS
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN BRATY, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BRATA, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BOTO ENGRED IN A SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BOTO ENGRED IN A SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BELLOO, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.4
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-39
PRIOR FILING DATE: 2000-06-30
PRI
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Bacher, Jeffery W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSES: Promega Corporation
STREET: 2800 Woods Hollow Road
CITY: Madison
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53711-5399
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09784423
Patent No. US20020012924A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 12; Conservative
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ORGANISM: Homo sapiens
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US-09-784-423-17
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A1531367 SD02371.5
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BH272267 1£28e01.y
BH019101 L2357k.d_
AV434035 AV434035
BM142008 1£25408.y
                                      (without alignments)
146.743 Million cell updates/sec
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                                 December 11, 2002, 16:56:23; Search time 1655.5 Seconds
                                                                                                                                                                                                                                                                                                                       Description
                                                                                                         32308132
     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                      16154066 seqs, 8097743376 residues
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                       - nucleic search, using sw model
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BM273267
BH019101
AV434035
BM142008
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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COMMENT Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 180 FEATURES FEATURES FOOTHORISH STATE STAT	Query Match 100.0%; Score 15; DB 14; Length 309; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 CCTTCTCGCCTGTT 15 Db 107 CCTTCTCGCCTGTT 93	RESULT 2 BH019102 LOCUS LOCUS BH019102 LOCUS DEFINITION L2358k.d_HygT3.1 Leishmania major Friedlin Cosmid Genomic Library ACCESSION BH019102 REVWORDS REYWORDS SOURCE Leishmania major CRANISM Leishmania major CRANISM Leishmania major CRANISM Eustryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.	REFERENCE 1 (bases 1 to 313) AUTHORS Wyler, P.J., VOGI, C., Cawthra, J., Klacking, M., Marty, A., Mack, J., Munden, H., Nguyen, D., Robertson, L., Sisk, E., Fazelinia, G., Aggarwal, G., Nelson, S., Seyler, A., Worthey, E. and Stuart, K. IIILE Leishmania major Friedlin Cosmid End Sequences JOURNAL Unpublished (2000) COMMENT Scattle Biomedical Research Institute 4 Nickerson Street, Seattle, WA 98109-1651, USA Tel: 206 284-8846 Fax: 206 284-8846 Tel: 206 284-8846 Tel: 205 284-8846 Tel: 205 284-8846 Tel: 305 284-8845 Tel: 305 384-8845 Tel: 305 384-8	/organism="Leishmania major" /strain="Friedlin" /db_xref="taxon:5664" /clone="L2358k" /clone_lib="Leishmania major Friedlin Cosmid Genomic Library" /lab_host="E. coli ED8767"
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RESULT 1 T48892/c LOCUS DEFINITION

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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Endocrine Pancreas Consortium
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Unliana Brown
Cbrown@fas.harvard.edu This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
AA 02138
Tel: 617-495-1812
Fax: 617-495-8557
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
/note="Vector: cLHYG; Site_1: BamHI; Genomic DNA from Leishmania major Friedlin was partially digested with Sau3AI. size selected, and ligated with BamHI-digested cLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivens et al., Genomics Research, 8:135-145 (1998). The CLHYG vector (Acc. No. CVUS9231) is described in Ryan et al, Gene, 131:145-150 (1993)"
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Other_ESTs: if28e01.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0;
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amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 513)
Myler, P.J., Vogr, C., Cawthra, J., Klacking, M., Marty, A., Mack, J.,
Munden, H., Ngyen, D., Robertson, L., Sisk, E., Fazelinia, G., Aggarwal
, G., Nelson, S., Seyler, A., Worthey, E. and Stuart, K.
Leishmania major Friedlin Cosmid End Sequences
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//lab_host="Vector: CLHYG; Site_1: BamHI; Genomic DNA from Leishmania major Friedlin was partially digested with Sau3AI, size selected, and ligated with BamHI-digested CLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivens et al., Genomics Research, 8:135-145 (1998). The CLHYG vector (Acc. No. CVU59231) is described in Ryan et al, Gene, 131:145-150 (1993).
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4 Nickerson Street, Seattle, WA 98109-1651, USA
Tel: 206 284-0313
                                                                                                                                                                                                                                                                                                                             Score 15; DB 13;
Pred. No. 1.8e+02;
0; Mismatches 0;
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llarity 100.0%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 0;
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/clone="L2357k"
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1. .513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mylerpjesbri.org
Seq primer: HygT3
Class: cosmid ends.
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Best Local Similarity 100.0%;
Matches 15; Conservative 0;
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Contact: Myler PJ
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Matches 15; Conserv
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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                                                                      Tel: 617-495-1812
Fax: 617-495-8557
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BF971415
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 551)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Emishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hiller, L., Marra, M., Pape, D., Wille, T., Marth, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,
M., Glbbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Endocrine Pancreas Consortium
L Onpublished (2000)
other_ESTS: if25408.11
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
                                                                                  543 bp mRNA linear EST 23-AUG-2000 AV434035 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PM037d06_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/clone_lib="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       if25d08.yl Melton Normalized Human Islet 4 N4 HIS 1 Homo sapiens con alone IMAGE:5677479 5' similar to SW:CAlE HUMAN P39059 COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1]; , mRNA sequence.
                                                                                                                                                                                                                                                                              Porphyra.
1 (bases 1 to 543)
Nikaido,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                         Porphyra yezoensis
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="TU-1"
/db_xref="taxon:2788"
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Best Local Similarity 100.
Matches 15; Conservative
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        52 CCTTCTCGCCCTGTT 66
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AV434035
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COMMENT

SOURCE

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FEATURES

TITLE

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/ncce="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hybrary.
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                             Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.lnl.gov High quality sequence stop: 414.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 617)
                                                                                                                                                                                                                                                                                    1. .551
//Organism="Homo sapiens"
/do_xref="taxon:9606"
/clone=IIM6E:5677479"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCS
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 t
Email: dmelton@biohp.harvard.edu
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human.
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                                                                                                                                                              /clone_lib="NHH_MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab.host="bH10B (phage-resistant).
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHLMGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 626)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zk87h09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE.489857 3' similar to SW:CAIE_HUMAN P39059 COLLAGEN ALPHA 1(XV AA10211)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. Insert Length: 867 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 617;
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H44 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                      Score 15; DB 12;
Pred. No. 1.9e+02;
0; Mismatches 0;
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Location/Qualifiers
http://image.llnl.gov
Plate: LLAM10003 row: c column: 09
                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4361024"
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/db_xref="GDB:3804444"
                                         High quality sequence stop: 614.
Location/Qualifiers
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/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÁA102111
AA102111.1 GI:1646031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 CCTTCTCGCCCTGTT 361
                                                                                      .617
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JOURNAL
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                                                                FEATURES
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Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 628)  

Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, M., Hawkins, M., Hultman, M., Kucabb, T., Leay, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zk87h09.rl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone NmAGE:489857 5' similar to SW:CAlE_HUMAN P39059 COLLAGEN ALPHA 1(XV AA099915
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library
                                                                                                                      Not
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                                                                              double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the No and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Final: est@wastl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 867 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality.sequence stop: 492.
Site_2: Eco RI; 1st strand cDNA was primed with a Not oligo(dT) primer {5'
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                            Length 626;
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/clone_lib="Soares_pregnant_uterus_NbHPU"
                                                                                                                                                                                                                                                                                                                                                                                  Indels
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100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
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Conservative (
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Best Local Similarity
Matches 15; Conserv
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constructed by M. Fatima Bonaldo."

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Best Local Similarity
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BE776197/c
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/organism="Chlamydomonas reinhardtii"
/strain="C-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II"
/note="Vector: pBluescript II SK'; Site_I: ECORI; Site_2:
/note="Vector: pBluescript II SK'; Site_I: Z4 hr;
/note="Vector: pBluescript II SK'; Site_I: Z4 hr;
/sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr)
/sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr)
/sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr)
/sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr)
/sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr)
/sorbitol 
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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Grossman, Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebv, F., McDermott, J. B., Shrager, J., Sliflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Notcellular System for Analyzing Gene Function and Regulation in Unpublished (2001)
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                                                                        Length 628
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
                                                                     100.0%; Score 15; DB 9; I
100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0;
122
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     σ
  189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                  Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                        252 CCTTCTCGCCCTGTT 238
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Matches 15; Conserv
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:316255"
/clone="IMAGE:316255"
/clone="IMAGE:316255"
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="nenin; Vector: pOTB7; Site_1: XhoI; Site_2: Note: Organ made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5/ adaptor: GGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NH-MGC Library."

25 a 203 c 166 g 165 t
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MY-12-B-02 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.
BE776197
BE313934 G59 bp mRNA linear EST 26-OCT-2000 601147310F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162555 5',
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                                                                                                                                                                                                                                        Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 659)
1MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM122 row: c column: 04
High quality sequence stop: 618.
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1 (bases 1 to 676)
Kamoun, S., Hraber, P.T., Sobral, B.W.S., Nuss, D. and Govers, F. Initial assessment of gene diversity for the comycete pathogen Phytophthora infestrans based on expressed sequences
Phytophthora infestrans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
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100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
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COMMENT
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/note="Vector:
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Best Local Similarity 100.
Matches 15; Conservative
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BG444893/c
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BQ609181
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/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/tab_most="NHIOB (phage-resistant)"
/lab_most="NHIOB (phage-resistant)"
/note="Organ: brain; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
                                                                                                                                                                                                                                                     Mayorlum in synthetic medium"

/lab_host="E. coli, strain DH5-alpha"

/note="Vector: pSpORTI; Site_1: Sall; Site_2: NotI; Total

/note="Vector: pSpORTI; Site_1: Sall; Site_2: NotI; Total

RNA was isolated from mycelium of P. infestans DDR7602

cultured for 4 weeks in synthetic medium. EST clones were

named by their position in the microtiter plate, preceded

by the prefix MY (for mycelial) and the successive number

of the microtiter plate (e.g. MY 06-A-04)."
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                 Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands rel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM1039 row: e column: 07 High quality sequence stop: 644.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                    /strain="DDR7602, Al mating type"
/db_xref="taxon:4787"
/clone_lib="PinfestansMY"
/dev_stage="4-week old vegetative, non-sporulating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 676;
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                                                                                                                                                   /organism="Phytophthora infestans"
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100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
                                                                                                             Location/Qualifiers
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Wageningen University
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Best Local Similarity
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BRY_5105 wheat EST endosperm library Triticum aestivum cDNA 5', mRNA sequence. BQ609181. GI:21558520 EST.
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Gossypium arboreum

Gossypium arboreum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosids II; Malvales; Malvaceae; Gossypium.

1 (båses 1 to 830)
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An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="AKA"
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/db_xref="taxon:99729"
/clone="GA_Ba0025919f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
                                                                                                                                Gaps
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116 t
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                                                                                 Length 713;
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this is a NIH_MGC Library."
59 c 203 g 152 t
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100.0%; Pred. No. 2e+02;
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0
                                                                                                     Pred. No. 1.9e+02;
                                                                               100.0%; Score 15; DB 12; ilarity 100.0%; Pred. No. 1.9e+02; Conservative 0; Mismatches 0;
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Clemson University
IOU Ordean Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Gossypium arboreum"
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Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 182.
Location/Qualiflers
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Liticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatorphyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticae; Tr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Triticum aestivum"
/cultivar="Wyuna"
/cultivar="Wyuna"
/db_xxef="taxon:4565"
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/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/note="Vector: Bluescript II SK(-)"
a 409 c 68 g 326 t
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100.0%; Score 15; DB 14; Length 839;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 0; Indels (
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bread wheat.
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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- nucleic search, using sw model	December 11, 2002, 12:26:07; Search time 1657 Seconds (without alignments) 263.453 Million cell updates/sec	US-09-750-609-9 ore: 15 1 ccttctcgccctgtt 15	ole: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	2054640 segs, 14551402878 residues	er of hits satisfying chosen parameters: 4109280	seq length: 0 seq length: 2000000000	Minim Maxim Listi	GenEmbl:* 1: gb_ba:* 2: gb_ba:* 4: gb_com:* 5: gb_par:* 7: gb_par:* 7: gb_par:* 8: gb_par:* 10: gb_pr:* 10: gb_pr:* 11: gb_cs:* 11: gb_cs:* 12: gb_cs:* 13: gb_cs:* 14: gb_cs:* 15: em_bar:* 16: em_bar:* 17: em_bar:* 18: em_bar:* 22: em_ov:* 23: em_ov:* 24: em_ph:* 25: em_ov:* 25: em_ov:* 26: em_ov:* 27: em_bar:* 28: em_br:* 29: em_br:* 21: em_br:* 22: em_ov:* 23: em_br:* 24: em_br:* 25: em_ov:* 25: em_ov:* 26: em_ov:* 27: em_br:* 28: em_br:* 29: em_br:* 20: em_ov:* 21: em_br:* 22: em_ov:* 23: em_br:* 24: em_br:* 25: em_ov:* 26: em_ov:* 27: em_br:* 28: em_br:* 29: em_br:* 30: em_br:* 31: em_br:* 32: em_br:* 33: em_br:* 34: em_br:* 35: em_br:* 36: em_br:* 37: em_br:* 38: em_br:* 39: em_br:* 30:
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PRI 06-JUL-2001

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S Bonisch, H.

S Bonisch, H.

Direct Submission
L Submitted (30-AUG-1995) H. Bonisch, Institut fuer Pharmacologie und Toxikologie, Universitaet Bonn, Reuterstr 2b, 53113 Bonn, FRG Related Sequences: M65105 and X57700.

Related Sequences: M65105 and X57700.

Location/Qualifiers
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I (bases 1 to 980)

Porzgen, P., Bonisch, H. and Bruss, M.
Molecular cloning and organization of the coding region of the Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. 215 (3), 1145-1150 (1995)
                                                                                                 Homo sapiens partial SLC6A2 gene for norepinephrine transporter,
                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 980)
Porzgen, P., Bonisch, H., Hammermann, R. and Bruss, M.
The human noradrenaline transporter gene contains multiple
polyadenylation sites and two alternatively spliced C-terminal
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norepinephrine transporter; SLC6A2 gene.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Chu/T., Blumenfeld,M. and Cohen,D.
Biallelic markers derived from genomic regions carrying genes
involved in central nervous system disorders
Patent: WO 0151659-A 104 19-JUL-2001;
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/note="16-2-76.mis2, complement"
240..260
/note="downstream amplification primer, complement"
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Patent: WO 0151659-A 99 19-JUL-2001;
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Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McClowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Unknown (protein for IMAGE:3162672)"
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PEAISTLSGSTFWAVVFFVWLLALGLDSSMGGMEAVITGLADDFQVLKRHRKLFTFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 5 Row: i Column: 7
                PRI 12-JUL-2001
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MMGPRPGLYWRLCWRFVSPAFLLFVVVVSIINFRPLTYDDYIPPPWANWYGWGIALSS
MVLPIYVIFYLSTGGSPAFLASTGITPENBHHLVAQRDIRQFQLQHWLAI"
378 c 356 g 373 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                       Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Homo sapiens, clone IMAGE:3162672, mRNA, partial cds.
BC000563
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                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                               BC000563.1 GI:12653576
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Matches 15; Conserv
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/product="noradrenaline transporter"
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1 (bases 1 to 1983)
Pacholczyk,T., Blakely,R.D. and Amara,S.G.
Expression cloning of a cocaine- and antidepressant-sensitive human noradrenaline transporter
Nature 350 (6316), 350-354 (1991)
2008212
         PRI 07-JAN-1995
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Myers, J.C., Kivirikko, S., Gordon, M.K., Dion, A.S. and Pihlajaniemi, T.
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Homo sapiens (library: gtll from Clonetech Laboratories) placenta
CDNA to mRNA.
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HUMNORTR 11near 1983 bp mRNA linear Human noradrenaline transporter mRNA, complete cds.
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100.0%; Pred. No. 6.6e+02;
iive 0; Mismatches 0;
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1. .1983
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noradrenaline transporter.
Human, CDNA to mRNA.
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/citation=[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kivirikko,S., Heinamaki,P., Rehn,M., Honkanen,N., Myers,J.C. and Philajaniemi,T.
Primary structure of the alpha 1 chain of human type XV collagen and exon-intron organization in the 3' region of the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 5161)
Myers,J.C., Kivirikko,S., Gordon,M.K., Dion,A.S. and
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Homo sapiens (tissue library: Clontech bases 955-5167) umbilical
cord (bases 1-954) cDNA to mRNA.
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triple-helical region
Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992)
93066196
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HOMO Sapiens alpha-1 type XV collagen mRNA, complete cds.
L25286
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583 c 644 g 392 t
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/tissue_lib="Clontech bases 955-5167"
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/citation=[2]
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INTPPTPSSPFEDMELSGEPVPEGTLETTNMSILOHSSPKQGSGELLMDTLEGVHSVD
GDPITDSGSGAGAFLDIAEEKNLAATAAGLAEVPISTAGEAEASSVPTGGPTLSMSTE
NPEEGVTPGPDNEERLKATAAGEAEALASMPGEVEASGVAPGELDLSMSAQSLGEEAT
                                                                                                                                                                                                                                                                                                          VGPSSEDSLTTAAAATEVSLSTFEDEEASGVPTDGLAPLTATVAAPERAVTSGFGDEED
AAATTEEPLITAGGEESGSPPPDGPPLPLPTVAPERMITPAQREHVGMKGQAGPKGE
KGDAGEELPGPPEPSGPPTGARAEAEGSGLGWGSDVGSGSCDLVGSBDLLRCPPGPP
GPPGLFGIPGRRGTPVRGPRAGAEAEGSGLGWGSDVGSGSCDLVGSBDLRCPPGPP
GPPGLFGIPGRRGTPGPPGFKKGQAGPPGPPGPPGGPPGGPRGEKG
ARGPNGSVGEKGDPGNRGLPGPPGKKGQAGPPGVPRGPPGGPPGGPPGGPPGBPGFF
DTEGSGSTQLLNEPKLSRPTAAIGLKGEKGDRGPKGERGMDGASIVGPPG
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QLIGDPLPSSVSFVTGYGGFPAYSFGPGANVGRPARTLIPSTFFRDFAIRLVVKPSST
                                                                                                                                                              WNRFAMIVQGEEVTLLVNCEBHSRIPPQRSSQALAFESSAGIFMGNAGATGLERFTGS
LQQLTVHPDPRTPEELCDPEESSASGETSGLQEADGVAEILEAVTYTQASPKEAKVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLIGIKGTKGIDDGVIMOGPPGIPGPFGPPGPPGAVINIKGAIFPIPVRPHCKNPVDTA
HPGSPELITHGVKGEKGSWGLPGSKGEKGDGAGPPGPPLDLAYLRHFLNNLKGEN
GDKGFKGEKGEKGDINGSFPENSGPPGLPGNPGPAGGKGETVVGPGQPPGPAGLGEPPG
FGRPGDPGPPGPALIGAAVALPGPPGPPGPPGLPGCSRNLYTAFSNNDMLO
KAHLVIEGTFIYLRDSTEFFIRVRDGWKKLQLGELIPIPADSPPPALSSNPHQLLPP
                                                                                                                                     RGGVLFAITDAFQKVIYLGLRLSGVEDGHQRIILYYTEPGSHVSQEAPAFSVPVMTHR
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EQGERGEPGAILTEDIPLERLMGKKGEPGMHGAPGPMGPRGPPGHKGEFGLPGRPGRP
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KVIWHGSSPHGVRLVDNYCEAWRTADTAVTGLASPLSTGKILDQKAYSCANRLIVLCI
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100.0%; Score 15; DB 9; Length 5161;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels (
type XV collagen"
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/note="putative"
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/label=mat-peptide
4254. .5161
/gene="COL15A1"
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165. .4253
/gene="COL15A1"
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/label=polyA_site
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4913. 4918
/gene="COL15A1"
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5126. .5131
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4407. .4412
/gene="COL15A1"
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/gene="COL15A1"
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/gene="COL15A1"
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                                                                                                                                            AC020425 14621 bp DNA linear HTG 03-JAN-2000 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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Mus musculus clone RP23-117121, LOW-PASS SEQUENCE SAMPLING.
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Birren B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kallas, A., Kells, C., Lexdine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Matthews, C.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 61956)
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10213135 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 14621)
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-117121
Upublished
O 'L---- 1 + A1956)
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/db_xref="taxon:7227"
2792 c 2769 g 4724 t
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HTG; HTGS_PHASE0.
Mus musculus.
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AC020425.1 GI:6664472
HTG; HTGS_PHASE2.
4882 CCTTCTCGCCCTGTT 4896
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McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, V., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viell, R., V., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Zahnou, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                   Submitted MANACON-2001) Whitehead Institute/MIT Center for Genome Submitted, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This record contains 79 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0280: gap of 100 bp 10969: contig of 689 bp in 11740: contig of 671 bp in 112509: contig of 669 bp in 12509: contig of 669 bp in 13254: contig of 645 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp
of 682 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 bp '
f 671 bp i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 100 bp
contig of 776 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54: gap of 100 bp
14028: contig of 674 bp
28: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L16579
Center clone name: 117_121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4: gap of
6290: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11069: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13354: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13255 13354: gap of
13355 14028: con
14029 14128: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9509: gap of
10180: cor
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9409: cor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12510 12609:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved.
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us-09-750-609-9.rge

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55 24254; gap of 100 bp 105 bp in length 15 25044; gap of 100 bp 105 bp in length 15 25047; contig of 660 bp in length 16 2597; gap of 100 bp 100 bp 16570; contig of 673 bp in length 16570; gap of 100 bp 100 bp 17328; contig of 673 bp in length 17 27328; contig of 678 bp in length 18 27428; gap of 100 bp 100 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 21107: gap of 100 bp 23 21952: contig of 745 bp in length 53 21952: gap of 100 bp 22 2535: contig of 683 bp in length 100 bp 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 28953: Contigo to 4, by in tength 105 2893: Contigo of 669 bp in length 14 273: gap of 100 bp 100 bp 13 30482: Contigo of 749 bp in length 13 30582: gap of 100 bp 100 bp 13 31343: Contigo of 761 bp in length 14 3143: gap of 100 bp 100 bp
                                                           14895: gap of 100 bp
15570: contig of 675 bp in length
15670: gap of 100 bp
16330: contig of 660 bp in length
16430: gap of 100 bp
17099: contig of 669 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18693 18792; gap of 100 bp 18793 19467; contig of 675 bp in length 19568 20238; contig of 671 bp in length 20239 20338; gap of 100 bp 100 bp 20239 20338; gap of 100 bp 20339 21007; contig of 669 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of 100 bp 103: contig of 704 bp in length 92: contig of 689 bp in length
      14795: contig of 667 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17: gap of 100 bp
28864: contig of 647 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34720: gap of 100 bp 35467: contig of 747 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p of 100 bp contig of 655 bp in length p of 100 bp contig of 676 bp in length
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41003: contig of 660 bp
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40243:
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38547:
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36222:
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Shren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Bodkhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collismore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galdgan, J., Gardyna, S., Ginde, S., Goyette, M., Graph, D., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Lindblad-Toh, K., Landers, T., Lehocsky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Wonsen, L., McCol, R., O'Donnell, P., O'Donnell, P., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petta, R., Ribes, C., Rogov, P., Roman, J., Rostett, M., Roy, A., Santos, R., Schauer, S., HTG 30-JUL-2002 Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 65851)
Birran, B. Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP13-519019 Gaps AC124280 65851 bp DNA linear HTG 30-JUI HOMO Sapiens chromosome 17 clone RP13-519019 map 17, LOW-PASS SEQUENCE SAMPLING. ; 0 100.0%; Score 15; DB 2; Length 61956; 100.0%; Pred. No. 6.5e+02; .ive 0; Mismatches 0; Indels 0 44852: contig of bob bp in length
44852: contig of 656 bp in length
44852: contig of 656 bp in length
44852: contig of 656 bp in length
28 4527: gap of 100 bp
28 46410: contig of 675 bp in length
46510: gap of 100 bp
11 46510: gap of 100 bp
18 47287: gap of 100 bp
8 48012: contig of 677 bp in length
18 47287: gap of 100 bp
13 48784: contig of 672 bp in length
13 48112: gap of 100 bp
18 58884: gap of 100 bp
18 58884: gap of 100 bp
18 58884: gap of 100 bp
19 665 bp in length
20 49649: gap of 100 bp
20 49649: gap of 100 bp
20 50 50388: contig of 665 bp in length 51872 51971: gap of 100 bp 51972 52651: contig of 680 bp in length 52652 52751: gap of 100 bp 52752 53427: contig of 676 bp in length 53428 53527: gap of 100 bp 53528 54200: contig of 673 bp in length 54200: gap of 100 bp contig of 669 bp in length gap of 100 bp 1: contig of 664 bp in length gap of 100 bp 6: contig of 666 bp 50438: gap of 51107: cont AC124280 AC124280.3 GI:22004380 HTG; HTGS_PHASE0. 44096: 51871: (bases 1 to 65851) Db 57817 CCTTCTCGCCCTGTT 57831 51207: Conservative 1 CCTTCTCGCCCTGTT 15 46511 47188 47288 48013 50339 51108 51208 51872 51972 Best Local Similarity Matches 15; Conserv 49550 numan. Query Match SOURCE ORGANISM LOCUS DEFINITION REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS RESULT 10 ACCESSION VERSION KEYWORDS AC124280 δ

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                                                                                                                                                                                        University Street Submission

Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 6581)

Biren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyn, C., Gandan, D., Gandan, J., Grand-Pierre, N., Hagos, B., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymon, C., Nicol, R., Nessil, Ev, H., Pesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Wilson, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Wold, R., Volle, R., Volle, R., Wilson, B., Stange-Thomann, N., Young, G., Zainoun, J., Viel, R., Wallson, B., Stange-Thomann, N., Young, G., Zainoun, J., Direct, Submission
Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 30, 2002 this sequence version replaced gi:21699374.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
------------- Project Information
Center project name: 1.27356
Center clone name: 519_0_19
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1543 1642: gap of 100 bp
1643 2336: contin 100 bp
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Web site: http://www-seq.wi.mit.edu
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6473:
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COMMENT

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AC009031 90280 bp DNA linear HTG 26-JAN-2000
Homo sapiens chromosome 16 clone RP11-13M21, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 90280)
Dioc Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Schome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA
On Jan 26, 2000 this sequence version replaced gi:5686044.
         /clone_lib="cr-1j6"
/clone_lib="cr-1j6"
/note="This is one of two clone in the same well cr-1j6"
14154 a 25825 c 24793 g 15894 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90280)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                        Length 80669;
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gap of unknown length
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unknown length
                                                                                                                                                      Score 15; DB 2; Pred. No. 6.5e+02;
                                                                                                                                                                                                 Mismatches
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Unpublished
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Center Code: JGI
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AC009031.2 GI:6758938
HTG; HTGS_PHASE0.
HOMO sapiens.
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Chlamydomonas reinhardtii clone cr-1j6, WORKING DRAFT SEQUENCE, 1
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Direct Submission
Submitted (14-AUG-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC130797.1 GI:22218470
HTGS. PHASE2; HTGS. DRAFT.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 80669)
Wu, H., Lin, S., Jia, H., Dutcher, S. and Roe, B.A.
Chlamydomonas reinhardtii BAC Clone cr-1j6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                    41044 41143: gap of 100 bp 41144 41859: contig of 716 bp in length 41860 41959: contig of 716 bp in length 41860 41959: contig of 724 bp in length 42784 42783: gap of 100 bp 44522 43621: contig of 738 bp in length 4352 43621: gap of 100 bp 4450 4459: contig of 738 bp in length 4350 4459: gap of 100 bp 4450 4459: gap of 100 bp 45198: gap of 100 bp 45198: gap of 100 bp 45198: gap of 100 bp 45299 46011: contig of 733 bp in length 45299
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              38578 38677. 386 of 100 bp in length 38678 39398: contig of 721 bp in length 39499 39499. gap of 100 bp 40210: contig of 712 bp in length 40311 40310: gap of 100 bp in length 4104 4143; gap of 100 bp in length 4104 4143; gap of 100 bp in length 41144 41859: contig of 716 bp in length
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/organism="Chlamydomonas reinhardtii"
/db_xref="taxon:3055"
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100.0%; Pred. No. 6.5e+02;
iive 0; Mismatches 0;
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9962: contig of 689 b gap of unknown 8478: contig of 742 b gap of unknown 9239: contig of 744 b gap of unknown 9239: contig of 743 b gap of unknown 12220: contig of 655 b gap of unknown 12289: contig of 655 b gap of unknown 12989: contig of 655 b gap of unknown 12989: contig of 655 b gap of unknown 13644: contig of 675 b gap of unknown 15914: contig of 613 b gap of unknown 15914: contig of 613 b gap of unknown 15914: contig of 613 b gap of unknown 16730: contig of 613 b gap of unknown 18738: contig of 613 b gap of unknown 18738: contig of 613 b gap of unknown 18738: contig of 625 b gap of unknown 20076: contig of 625 b gap of unknown 20064: contig of 613 b gap of unknown 20064: contig of 613 b gap of unknown 24364: contig of 625 b gap of unknown 25674: contig of 625 b gap of unknown 25891: contig of 773 b gap of unknown 25891: contig of 77 b gap of unknown 25891: contig of 77 b gap of unknown 27382: contig of 77 b gap of unknown 29243: contig of 770 b gap of unknown 29243: contig of 770 b gap of unknown 30770: contig of 1046 b gap of unknown 30770: contig of unknown 30770: contig of 1046 b gap of unknown 30770: contig of 1046 b gap of unknown 30770: contig of 1046 b gap of unknown 30770: contig of	* 3373(*	* 3380	* 3477(* 3556	* *	* 1	* 3/1/5	* 38598	* 3940(* 40533	* 4161; *	* 42658 *	* 43645	* 44809	* 46148 *	* 47218 *	* 48523 *	* 4931(*	* 50844 *	* 52194 *	* 53318 *	* 54464 *	* 55712 *	* 56684 *	* 5821(*	* 59764 *	* 61210	* 62916	* 64135	* 65999	* 67326 *	* 68611 *	* 70087 *	* 71289 *	* 73311	* 74255	
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	6274	1000	7/35	84 / 9	9240	9983	10642	11389	12221	12990	13645	14447	15321	15915	16671	17492	18136	18739	19364	20077	.20850	22065	23061	23684	24345	24970	25268	25892	26675	27383	27460	28326	29244	30010	30771	31473	1

gap of unknown length of 1202 bp in length funknown length of 2022 bp in length unknown length of 948 bp in length funknown length of 1578 bp in length unknown length bp in length length bp in length length bp in length length unknown of 1327 unknown unknown contig c gap of c contig c gap of c contig c contig gap of contig gap of contig gap of contig gap of 34775: 36526: 68610: 37178: 33804: 35568: 38597: 39399: 40532: 41611: 42657: 43644: 44808: 46147: 47217: 48521: 49309: 50843: 53317: 54463: 55711: 56683: 58209: 59763: 62915: 64134: 73310: 52193: 61209: 65998: 67325: 70086: 71288: 74258: 75836: 35 00 33 60 22

Length 90280;

DB 2;

Score 15;

100.08;

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us-09-750-609-9.rge

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Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Polubokan, I., Pu, L.L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Shooshtari, N.,
Sisson, I., Sodergen, E., Sonaike, T., Sparks, A., Stanley, H.,
Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, M.,
Tang, H., Tansey, J., Taylor, C., Taylor, T., Taplero, B., Thomas, N.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.,
Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Weilington, S., Williams, G., Williamson, A., Wleezyk, R., Wooden, S.,
Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Direct Submission Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K.C.
Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TY 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15624602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: Estimated insert size may differ from sequence length

* See http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 65 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* truns of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GBID
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Rattus norvegicus clone CH230-5L5, *** SEQUENCING IN PROGRESS ***,
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                                                                                                          contig of 2962 gap of unknown contig of 2182 gap of unknown contig of 2201 gap of unknown contig of 2396 gap of unknown contig of 1872 gap of unknown contig of 1873 gap of unknown contig of 1874 gap of unknown contig of 1875 gap of unknown contig of 1876 gap of unknown contig of unknown 
                                                                                                                                      of 1338 k
unknown 1
of 2182 b
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unknown of 1820 h
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16075)
Chu,T., Blumenfeld,M. and Cohen,D.
Biallell: markers derived from genomic regions carrying genes
involved in central nervous system disorders
Patent: WO 0151659-A 544 19-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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/note="199-32148-315.mis complement"

31844. 31862

34799. 334930
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Pred. No. 6.5e+02;
0; Mismatches 0;
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31528. 31546
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                      of 1252
unknown
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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138283:
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KEYWORDS
SOURCE
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TITLE
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primer_bind

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variation 67963

variation 67963

primer_bind 67964..67982

primer_bind 68051..68070

BASE COUNT 43057 a 36601. 38189 g 42727 t 181 others

Ouery Match

Best Local Similarity 100.0%; Score 15; DB 6; Length 160755;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

Db 63345 CCTTCTCGCCCTGTT 63359

Search completed: December 11, 2002, 14:35:19

Job time: 1782 secs
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December 11, 2002, 12:23:57; Search time 212.5 Seconds (without alignments) 158.965 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Probe for human no CNS disorder-relat CNS disorder-relat Nucleotide sequenc DNA encoding novel Nucleotide sequenc Nucleotide sequenc Human norepinepher Human cDNA differe Description SUMMARIES AAH88264 AAH88264 AAH28088 AAS80746 AAH28082 AAH28086 AAH28086 AAH28084 ΩI Query Match Length DB 1044 1854 1854 1983 5161 100.0 100.0 100.0 100.0 100.0 100.0 0.001 Score 15 115 115 115 115 115 Result No. O O

Human DNA sequence Human ORFX polynuc Human ovarian anti C glutamicum codin Drosophila melanog Tea gene (cDNA 20. T-cell transmembra Human T-cell early	on e or	Probe #25526 used Human genome-deriv Homo sapiens TSR r Human nervous syst Human ORFX polynuc		C 0 C -1
ААН88704 ABN18096 ABQ56203 AAH65499 ABL11823 AAQ14533 AAQ63614 AAV59846	ABL11822 AAH68525 AAH28085 ABA40720 AAK24835	AA156840 ABS24326 AAV27204 ABA15500 ABN17269 ABN24354	AAC00241 AAK69418 AAK69419 ABA11654 ABA11693 AAK57066 AAQ11640	AAN 2003 77 AAN 2003 77 AAN 2003 77 AAN 2003 70 AAN 2003 80 AAN 2004 AAN 2005 AAN 20
22 5 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7	22223	22 22 24 24 24	222222	200 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
160755 336 655 708 2036 2397 2397 2397	5031 349980 15 114 114	114 324 328 331	3372 3374 3374 400 411	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
100.0 93.3 93.3 93.3 93.3 93.3				000000000000000000000000000000000000000
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10 11 12 13 14 15 16	18 19 20 21 22	2222 2225 2425 243	333350 33350 3350 3570 3570 3570 3570 35	0 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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ALIGNMENTS

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Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine;
                                                                             Probe for human norepinephrine transporter gene wild type allele.
                  BP.
                                                                                                                     amphetamine abuse; probe; ss.
                                                                                                                                                                                                  28-DEC-2000; 2000WO-US35491.
                                                                                                                                                                                                                      29-DEC-1999; 99US-0173682.
11-JAN-2000; 2000US-0175456.
                  AAH28084 standard; DNA; 15
                                                          (first entry)
                                                                                                                                                                                                                                                                        В.
                                                                                                                                                                                                                                                    (UYVA-) UNIV VANDERBILT
                                                                                                                                                                                                                                                                                            WPI; 2001-425681/45.
                                                                                                                                                            WO200148246-A1.
                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                        Robertson D,
                                                         05-SEP-2001
                                                                                                                                                                                05-JUL-2001.
                                      AAH28084;
RESULT 1
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Screening for susceptibility to sub-optimal norepinephrine transport,

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                                                                              The present sequence represents a probe for the wild type allele of a human norepinephrine transporter gene. The specification a method for screening for susceptibility to sub-optimal norepinephrine transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for transporter genes are useful for gene therapy for modulating norepinephrine transport in a target cell and treating susceptibility to receive the subject to orthostatic incolerance.
                                                                                                                                                                                                                                                                      to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single nucleotide polymorphism; SNP; biallelic marker; human; ds; central nervous system disorder; CNS; NET; norepinephrine transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to biallelic markers derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker -
                                                                                                                                                                                                                                                                                                         hypertension, heart disease, psycho stimulant abuse e.g. cocaine or
particularly orthostatic intolerance in a subject by detecting a
polymorphism of norepinephrine transporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 15; DB 22;
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 0 A; 7 C; 2 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                 Claim 15; Page 69; 133pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH88259 standard; DNA; 920 BP
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Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                           amphetamine abuse.
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genes involved in central nervous system (CNS) disorders. The present sequence is one such biallelic marker derived from human norepinephrine transporter (NET) gene. This marker has a single nucleotide polymorphism (SNP) and is useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to biallelic markers derived from human genes involved in central nervous system (CNS) disorders. The present sequence is one such biallelic marker derived from human norepinephrine transporter (NET) gene. This marker has a single nucleotide polymorphism (SNP) and is useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single nucleotide polymorphism; SNP; biallelic marker; human; ds; central nervous system disorder; CNS; NET; norepinephrine transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker.
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker -
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/standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS disorder-related biallelic marker #15 from NET gene.
                                                                                                                                         Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;
                                                                                                                                                                             100.0%; Score 15; DB 23; 100.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                               Mismatches
                                                                                                      least one CNS disorder related marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                     AAH88264 standard; DNA; 920 BP.
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                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
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misc_feature
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                                                                                                                                                                                                                                                                                                                                      RESULT 3
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The present sequence represents exon 9 of the human norepinephrine transporter gene. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject. The method comprises obtaining a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful for gene therapy for modulating to impaired norepinephrine transporter (and transporter genes are useful for gene therapy for modulating to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, harbert size on the subsection or stimulant abuse e.g. cocaine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mental illness; hypertension; heart disease; stimulant abuse; cocaine; amphetamine abuse; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of a exon 9 of norepinephrine transporter gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norepinephrine transporter; orthostatic intolerance; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 980 BP; 218 A; 275 C; 246 G; 238 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 125; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                    AAH28088 standard; DNA; 980 BP
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11-JAN-2000; 2000US-0175456.
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257..700
/*tag= b
701..802
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                                     170 CCTTCTCGCCCTGTT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..257
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1 CCTTCTCGCCCTGTT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                  AAH28088
                                                                                                                                                                                RESULT
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or administrating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cappositic odding sequences of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human capping, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1044 BP; 229 A; 303 C; 258 G; 254 T; 0 other;
                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #16550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 16550; 103pp; English.
                                                                                                  )746/c
AAS80746 standard; cDNA; 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                              (first entry)
230 CCTTCTCGCCCTGTT 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73
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les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABG16559
                                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2.
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                                                                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001
                                                                                                                                                      AAS80746;
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                                                                                                AAS80746/
                                                                              RESULT 5
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Gaps

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0; Mismatches

Best Local Similarity 100. Matches 15; Conservative

Query Match

100.0%; Score 15; DB 22; Length 980; 100.0%; Pred. No. 1.8e+02;

AAH28082;

RESULT 6

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AAH28082

Key

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The present sequence encodes a human norepinephrine transporter. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful for gene therapy for modulating norepinephrine transport in a target cell and treating susceptibility to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as methal illness, hypertension, heart disease, psycho
                                                                                                                                                                                                                Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
                                                                                                                                                                   Nucleotide sequence of a human norepinephrine transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "norepinephrine transporter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 75; Page 112-115; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..1854
/*tag= a
                          AAH28086 standard; DNA; 1854 BP
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11-JAN-2000; 2000US-0175456.
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                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blakely RD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                amphetamine abuse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-425681/45.
P-PSDB; AAB84534.
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                         05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2001
                                                                           AAH28086;
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AAQ28118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a human norepinephrine transporter. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the subject to the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful for gene therapy for modulating norepinephrine transport in a target cell and treating susceptibility to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, hypertension, heart disease, psycho
                                                                                                                                                                                                                                                                                                 Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene .
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                                                                                                                                                                                                                                                      Nucleotide sequence of a human norepinephrine transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "norepinephrine transporter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stimulant abuse e.g. cocaine or amphetamine abuse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 75; Page 98-101; 133pp; English
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                                                                                                               AAH28082 standard; DNA; 1854 BP.
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11-JAN-2000; 2000US-0175456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blakely RD;
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97 CCITCTCGCCCTGTT 83
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                                                                                                                                                                                                                                                                                                                                                 amphetamine abuse; ss.
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P-PSDB; AAB84532.
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Best Local Similarity
Matches 15; Conserv
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                                                                                  Length 1854;
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                                      Sequence 1854 BP; 357 A; 553 C; 494 G; 450 T; 0 other;
stimulant abuse e.g. cocaine or amphetamine abuse.
                                                                              100.0%; Score 15; DB 22; 100.0%; Pred. No. 1.8e+02;
                                                                                                                        Mismatches
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RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                           NT; noradrenaline; neuroblastoma; neutotransmitter; antidepressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementary DNA clone encoding human norepinephrine transporter protein - isolated from human neuroblastoma cells and useful for determining action of e.g. antidepressant drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pools of clones from a human SK-N-SH cell (a human neuroblastoma cell line) cDNA library were transfected into COS-1 cells. The transfected clones were in the form of expression vectors (pXM) having an SV-40 replication origin to enable amplification. Transfectants of these cells expressing the norepinepherine transporter were identified by employing an assay exploiting the fact that the norepinepherine analogue m-iodobenzylguanidine (m-I is accumulated intracellularly by SK-N-SH cells expressing the intact NT. The accumulated radiolabelled m-IBG allows direct autoradiographic visualisation of transporter expressing the contract of the statement of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     name cell. Such studies include the relative effects of various psychotropic) drugs such as antidepressants.
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                                                                                Human norepinepherine transporter protein cDNA clone.
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                                                                                                                                                                                                                                                                                    Location/Qualifiers
61..1914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-US01376.
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                          15-MAR-1993 (first entry)
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ses 15; Conservative
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                                                                                                                                                                                                                               Homo sapiens
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ABK83862/c
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level in an unactivated the expression level in an unactivated at the expression level in an unactivated (GC, where differential expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GCA with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially charters the expression of at lergic response in a subject. exposure of a subject to a pathogen or sterile inflammatory disease using the charter of a subject to a pathogen or sterile inflammatory disease, by detecting the charter of expression in a sample of the tissue of gene(s) from GS, where the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation.

(4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or contacting an inflammation (especially chronic) or from GS, M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (as prometrial infection, viral infection, contacting or capable of modulating GCA preferably in an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (comparative of a subject to a pathogen or sterile inflammatory disease (comparative of a subject to a pathogen or sterile inflammatory disease, also bacterial infection viral infection, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
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                                                                                             Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                   Human cDNA differentially expressed in granulocytic cells #433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weissman SM, Yamaga S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2001; 2001WO-US30821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2000; 2000US-237189P
14-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-435328/46.
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes involved in central nervous system (CNS) disorders (see MAH88161-AAH88702). The markers have a single nucleotide polymorphism (SNP) and are useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker. The present sequence was used to illustrate the invention.
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to biallelic markers derived from human
                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 160755;
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0
                   Length 5161;
                                                                                                                                                                                                       Single nucleotide polymorphism; SNP; biallelic marker; human;
Sequence 5161 BP; 1254 A; 1420 C; 1363 G; 1124 T; 0 other;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                  100.0%; Score 15; DB 24;
11larity 100.0%; Pred. No. 1.9e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 15; DB 23; 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 476-519; 519pp; English.
                                                                                                                                                                                                                central nervous system disorder; CNS; ds
                                                                                                                          AAH88704 standard; DNA; 160755 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABN18096 standard; cDNA; 336 BP
                                                                                                                                                                                                                                                                                                                                                        Cohen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                     Human DNA sequence SEQ ID 544
                                                                                                                                                                                                                                                                                             11-JAN-2001; 2001WO-IB00116
                                                                                                                                                                                                                                                                                                                 13-JAN-2000; 2000US-0175854
                                                                                                                                                               26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 63345 CCTTCTCGCCCTGTT 63359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                  2673 CCTTCTCGCCCTGTT 2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                       1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                      Chu T, Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCTTCTCGCCCTGTT
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483085/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                      WO200151659-A2
                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 - JUN - 2002
                                     15;
                                                                                                                                                                                                                                                                         19-JUL-2001
                                                                                                                                              AAH88704;
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                                     Matches
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                                                                                                       RESULT 1(
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 on the specification). ABM15762 to ABM2722 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated Gisorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, intrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ cransplantation, cardiovascular diseases, disorders, infectious storage disease, various immune deficiencies and disorders, infectious disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also constitute for treating burns, incisions, ulcers, for treating osteoporosis, bone degeneration and treatment of lung or liver fibrosis, reperfusion in the constitution in the constitutions resulting from constitutions constitutions resulting from constitutions and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                  cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism, cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human polypeptides and polynucleotides useful for diagnosing,
                                                                      Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage degenerative disorder; osteoarthritis; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 336 BP; 61 A; 101 C; 109 G; 64 T; 1 other;
Human ORFX polynucleotide sequence SEQ ID NO:4669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                               myasthenia gravis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CTICTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 CTTCTCGCCCTGTT
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Les 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200192523-A2.
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 93% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens and the use of ovarian antigen polynucleotides and polypeptides in diagnosing. Irrating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system clasorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorihoea, endocrine disorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), brother and anomalia, cardiovascular disorders, conservations (e.g., congenital and acquired characters (e.g., condensed the conditions of the conditio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the factification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, frug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                                                                                                                                                   ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                          ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                               Human ovarian antigen HVVAW26 cDNA, SEQ ID NO:2083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 2083; 2922pp; English.
                            ABQ56203 standard; cDNA; 655 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-2001; 2001WO-US18569.
                                                                                                                                                   22-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurological diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-147878/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2002.
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                                                                                       ABQ56203;
                                                                                                                                                                                                                                                                             Human:
ABQ56203/
ID ABQ5
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashi M, Ochiai K, Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                         Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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0
                                                                                    Length 655;
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                                                                                                                     Indels
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                                                  12 other;
                                                                                                                                                                                                                                                                                                                                                                         C glutamicum coding sequence fragment SEQ ID NO: 534.
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                                                                                                  Pred. No. 5.8e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.3%; Score 14; DB 22; 18est Local Similarity 100.0%; Pred. No. 5.8e+02; Matches 14; Conservative 0; Mismatches 0;
                                                                                  DB 24;
                                                 Sequence 655 BP; 182 A; 168 C; 177 G; 116 T;
                                                                    93.3%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                        BP.
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2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                          organic acid synthesis; ds
                                                                                                                                                                                                                                                                                                                                      26-SEP-2001 (first entry)
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                                                                                                  Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                     2 CTTCTCGCCCTGTT 15
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                                                                                                                                                                                    556 CTTCTCGCCCTGTT
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03-AUG-2000;
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Tateishi N,
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                                                                                                                                                                                                                                                                                                        AAH65499;
                                                                                    Query Match
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                                                                                                                                                                                                                                       RESULT 13
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Location/Qualifiers 410..1767 /*tag= a

90WO-U002518 90US-0509684

DEV FOUND

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Multiple membrane spanning protein; T cell; development; ss.
                                                                                                                                                                                                                                                                                                                   New recombinant polypeptide comprising a T-cell protein regulate T-cell development and tumorigenic phenotype and block T-cell activation in auto:immune disease
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 13; 98pp; English
           Tea gene (cDNA 20.5).
                                                                                                                                                                                                                                                                                WPI; 1991-339818/46.
P-PSDB; AAR14645.
                                                             Mus musculus
                                                                                                                                                                                 12-APR-1990;
                                                                                                                                                                                                           13-APR-1990;
                                                                                                                                                                                                                                  (REDE-) RES
                                                                                                                                  WO9116430-A
                                                                                                                                                           31-OCT-1991
                                                                                                                                                                                                                                                         Macleod CL;
                                                                                   Key
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL130511), expressed DNA sequences (ABL16176-ABL130511), expressed DNA (ABB57737-ABP22072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                 Drosophila melanogaster expressed polynucleotide SEQ ID NO 29951.
                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.3%; Score 14; DB 23; Length 2036; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 29951; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2036 BP; 552 A; 513 C; 553 G; 418 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
                                                                                        ABL11823 standard; cDNA; 2036 BP
                                                                                                                                                                                                                                                                                                                                                                                       PWD,
                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231
                                                                                                                                         (first entry)
                                                                                                                                                                                                      pharmaceutical; gene; ss.
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     Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABB67720
                                                                                                                                                                                                                                                    WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions -
                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                          27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
                                                                                                                 ABL11823;
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                                                                  RESULT 14
                                                                              ABL11823
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                 specification.
The 20.5 gene, also referred to as Tea, identifies transcripts found in only a limited number of tissues. Tea transcripts are induced in splenocytes activated with the T cell mitogen ConA. Unlike other known genes expressed in activated T cells, the Tea gene appears to encode a protein which traverses the membrane multiple times, whereas the large number of known integral membrane protein which are induced in T cell activation are single membrane spanning proteins.
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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The 23 Ns in the sequence represent bases illegible in the
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                                                                                                                                                                                                                                                                    Sequence 2397 BP; 541 A; 570 C; 579 G; 684 T; 23 other;
                                                                                                                                                                                                                                                                                                                        DB 12; L 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: December 11, 2002, 13:38:15
Job time: 241.5 secs
                                                                                                                                                                                                                                                                                                                        Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                     93.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                      See also AAQ14530-34
                                                                                                                                                                                                                                                                                                                                                                                                                      2 CTTCTCGCCCTGTT
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserv
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Gaps

; 0

Matches 14; Conservative

ŏ a AAQ14533 standard; DNA; 2397 BP.

RESULT 15

AAQ14533 ID AAQ1

(first entry)

29-JAN-1992

AAQ14533;

Sequence 6, Appli Sequence 2, Appli Sequence 76, Appli Sequence 76, Appli Sequence 1, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli

Sequence Sequence Sequence

Sequence

Sequence 108, App Sequence 1, Appli Sequence 12, Appl Sequence 18, Appl

sequence Sequence

OM nucleic

Run on:

Sequence:

Searched:

Database

Result о В

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Sequence 5, Application US/07686322A
Patent No. 5312733
GENERAL INFORMATION:
APPLICANT: MacLeod Dr., Carol L.
TITLE OF INVENTION: No. 5312733el T-cell Lymphoma cDNA Clones
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Department, Fulbright & Jaworski
STREET: 1301 McKinney, Suit 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Texas
COUNTRY: USA
ZIP: 77010-3095
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                   US-09-491-522-6
US-09-491-522-2
US-09-171-337A-4
US-08-261-206A-76
US-09-254-325-1
                                                                                                                                                                                     US-09-491-522-1
US-08-306-691B-19
PCT-US93-06251-19
                                                                                                                                                                                                                                                                                                                                 US-08-094-079-12
US-08-094-079-18
US-08-094-079-20
US-08-094-079-22
                                                                                                                                                                                                                                                                US-09-177-650-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Launer, Charlene A.
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: D-5232-CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/686,322A FILING DATE: 19910411
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/509684
FILING DATE: 13-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell line
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INDIVIDUAL ISOLATE: SL12 cell
TISSUE TYPE: Lymphoma
CELL TYPE: T-cell
CELL LINE: SL12.3 and SL12.4
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (713) 651-3634
TELEFAX: (713) 651-5246
TELEX: WESTERN UNION 762829
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
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  Sequence 5, Appli
Sequence 5, Appli
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Sequence 29, Appl
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                                                                                                                                                                                        (without alignments) 97.876 Million cell updates/sec
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Sequence 1,
Sequence 22,
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                                                                                                                                                             December 11, 2002, 13:29:32; Search time 47 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: /cgg_2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                      GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-002-999-5
US-08-132-990A-5
PCT-US92-09382-5
PCT-0892-065A-137
PCT-US95-10398-137
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US-09-105-37-9
US-08-961-527-320
US-09-320-878-24
US-08-50-766-2
US-08-69-766-2
US-08-979-496-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-281-481A-18
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US-09-103-840A-1
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US-08-927-597-29
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                                                                                                                                                                                                                                                                                                                                                                                                                             441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                  - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                    US-09-750-609-9
15
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4411529
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Match Length
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                                                                                                                                                                                                                                                                                    Perfect score:
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APPLICANT: WERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Pred. No. 84;
+ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: FLORPY disk
COMPUTER: IBM PC Compatible
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,990A
FILING DATE: 07-07-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/899,075
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/899,075
FILING DATE: 11-JUN-1992
PRIOR APPLICATION NUMBER: 07/806,178
FILING DATE: 13-DEC-1991
PRIOR APPLICATION NUMBER: 07/627,950
FILING DATE: 14-DEC-1990
ATTORNEY/AGRAT INPORMATION:
NAME: MISCOCK, S. Leslie
REGISTRENCE/DOCKET NUMBER: 8105-004-9999
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 5, Application PC/TUS9209382 ; GENERAL INFORMATION:
                                                                             Sequence 5, Application US/08132990A; Patent No. 5834589; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 6641 PENNIE
INFORMATION FOR SED ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.3
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 1379 CTTCTCGCCCTGTT 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410..1768
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U:
ZIP: 10036
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US-08-132-990A-5
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PCT-US92-09382-5
                                                   US-08-132-990A-5
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                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08002999
Patent No. 5440017
GENERAL INFORMATION:
GENERAL INFORMATION:
AGLECOM MACLEOD Dr., Carol L.
TITLE OF INVENTION: No. 5440017el T-cell Lymphoma cDNA Clones NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Department, Fulbright & Jaworski
STRRET: 1301 McKinney, Suite 5100
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                DB 1; Length 2397;
84;
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                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUW TYPE: FIDPOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,999
FILING APPLICATION S30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,322
FILING APPLICATION NUMBER: US 07/686,322
FILING APPLICATION NUMBER: D-5232-DIV
REGISTRATION NUMBER: D-5232-DIV
TELEFRENCE/DOCKET NUMBER: D-5232-DIV
TELEFRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D-5232-DIV
TELEFRAX: (713) 651-5587
TELEFRAX: G13) 651-5587
TELEFRAX: G13
TELEFR
                                                            93.3%; Sco.
100.0%; Pred. No. c.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE: Lymphoma CELL TYPE: T-cell CELL LINE: SL12.3 and SL12.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                          Query Match 93.3
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.3
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: AKRI Jackson
INDIVIDUAL ISOLATE: SI
TISSUE TYPE: Lymphoma
                                                                                                                                                                                                                          1379 CTTCTCGCCCTGTT 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1379 CTTCTCGCCCTGTT 1392
                                                                                                                                                                                             2 CTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CTICICGCCCTGIT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 77010-3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: 20.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Texas
; CLONE: 2
US-07-686-322A-5
                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-08-002-999-5
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STATE:
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ANTICLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.4; DB 2; Length 573; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.6e
; Mismatches
                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
ITELERAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
15-AUG-1994
115-AUG-1994
118-AUG-1994
118-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 137, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 ALGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC COMPATIBLE SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: MORGAN & FINNEGAN
345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: S2
US-08-290-665A-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MUCITITEE OF INVENTION: AMINITIEE OF INVENTION: CORE TITLE OF INVENTION: AND MITHE OF INVENTION: SEQUENCES: 263 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 CCTTCTTGCCCTGTT 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCTTCTCGCCCTGTT 15
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                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK STATE: NEW YORK
                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10154
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STREET: 34
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                              APPLICANT: YOSHIMOTO, TAKAYUKI
IITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding
IITLE OF INVENTION: Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2397;
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Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: CORE GENES OF ISOLATES OF
TITLE OF INVENTION: CORE GENES OF ISOLATES OF
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC ME,
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC ME,
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.3%; · Score 14; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09382
FILING DATE: 19921213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MERUELO-1
                                                                                                                                 E: Browdy and Neimark
419 Seventh Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: MERUF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-5197
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
          MERUELO, DANIEL
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                          NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CTTCTCGCCCTGTT 15
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410..1768
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STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                             STREET: 419 server
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-08-290-665A-137
                                                                                                                                                                                                                                      20004
                                                                                                                                 ADDRESSEE:
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LOCATION:
PCT-US92-09382-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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Gaps

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Gaps
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PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
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      Score 13.4; DB 3; Length 630;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.3%; Score 13.4; DB 4; Length 630; 93.3%; Pred. No. 1.66+02; live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLACTACCATON
                                                                                                                                                                                                                                                 APPLICANT: MAERTENS, GEERT
APPLICANT: BARNAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BE WARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-NGE
TITLE OF INVENTION: PROTEINS FOR DIAG
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFAX: CANANTENESTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            RESULT 8
US-08-927-597-29
; Sequence 29, Application US/08927597
; Detent No. 6.445503
; GENERAL INFORMATION:
      89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                      Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 93.3
Matches 14; Conservative
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; LOCATION: 1..624
US-08-927-597-29
                                                                                                      177 CCTTCTCGCTCTGTT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 CCTTCTCGCTCTGTT 191
                                                                                  1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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LOCATION:
        Query Match
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APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARTWOFF, CONSTITUTION OF TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                       Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUMPRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25 (EPO)
RAPLICATION UDATA: (2/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                   Score 13.4; DB 5;
Pred. No. 1.6e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/08612973
Patent No. 6150134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFLICATION: 4.3.3
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487
TELECOMMUNICATION INFORMATION:
TELEPRONE: (703) 816-4100
INFORMATION FERENCE (703) 816-4100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                        137:
                                                                                                                                                                                                                                   89.3%;
93.3%;
TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
                                                                                                                                                      ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S2
PCT-US95-10398-137
                                                                                                                                                                                                                                 Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                   531 CCTTCTTGCCCTGTT 545
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                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               1 CCTTCTCGCCCTGTT 15
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                                                                                                                    linear
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                                                                                                                  TOPOLOGY: lin
ORIGINAL SOURCE:
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LOCATION:
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; LOCATION:
US-08-612-973-29
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSED: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Fatent No. 617659
GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: METACH, Mary C.
APPLICANT: MEDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.4; DB 4; Length 1475;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: CIP OF 09/141,908 EARLIER FILING DATE: 1998-08-28 EARLIER APPLICATION NUMBER: CIP OF 09/073,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: MSDOS version 6.2
                                                                                                   RESULT 11
US-08-961-527-320/c
; Sequence 320, Application US/08961527
; Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 320:
SEQUENCE CHARACTERISTICS:
LENGTH: 1475 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
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93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
                       246 CCTCCTCGCCCTGTT 260
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STRANDEDNESS: double
  1 CCTTCTCGCCCTGTT 15
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US-08-961-527-320
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US-09-320-878-24
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CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 738
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US-09-105-537-9
Sequence 9, Application US/09105537A
Sequence 9, Application US/09105537A
Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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Pred. No. 1.6e+02;
0; Mismatches 1;
                                    Sequence 747, Application US/09605785
Patent No. 6321716
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LENGTH: 1458
TYPE: DNA
CREANISM: Streptomyces venezuelae
US-09-105-537-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; LOCATION: (1)...(738)
; OTHER INFORMATION: n=A,T,C or G
US-09-605-785-747
                                                                                               APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                  Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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                                                                                                                                                                                                                                                                                                       Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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                                                                                                                                                                                                                                             Fanger, Gary R.
Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.3
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                   Stolk, John A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        Li, Samuel
                                                                                GENERAL INFORMATION:
RESULT 9
US-09-605-785-747/c
                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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APPLICANT:
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APPLICANT:
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APPLICANT: MORRISON, Nigel A
APPLICANT: BISAN, John A
APPLICANT: ELSAN, John A
APPLICANT: KELLY, Paul J
TITLE OF INVENTION: Assessment of Trans-Acting Factors Allelic
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.4; DB 1; Length 2169;
Pred. No. 1.70+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                               Length 1954;
                                                                                                                                                                                                                                                                                                                            Score 13.4; DB 3;
Pred. No. 1.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Rothwell, Figg, Ernst & Kurz STREET: Suite 701-E, 555 13th Street.N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 11, 2002, 15:30:43 Job time: 52 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/379,496
FILING DATE: 02-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENI INFORMATION:
NAME: ERNST, BATDAIR G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-114
EARLIER APPLICATION NUMBER: 60/012,600 EARLIER FILING DATE: 1996-03-01 NUMBER OF SEQ ID NOS: 22 SOFTWARE: PALENTIN Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08379496 Patent No. 5593833 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                  89.3%;
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93.3%;
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LENGTH: 2169 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double
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STRANDEDNESS: doubl
                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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US-08-379-496-1/c
                                                                                                                                                                      LENGTH: 1954
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                   US-08-922-635-2
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19.89-92-635-2/C

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29.89-92-635-36

29.89-92-635-2/C

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APPLICANT: PILETZ, John E.
APPLICANT: PILETZ, John E.
APPLICANT: PILETZ, John E.
APPLICANT: IVANOV, Tina R.
TITLE OF INVENTION: METHOD FOR CLONING A HUMAN IMIDAZOLINE RECEPTOR AND TITLE OF INVENTION: METHOD FOR CLONING THE SAME FILE OF INVENTION: METHOD FOR CLONING THE SAME TITLE OF INVENTION: METHOD FOR CLONING THE SAME CURRENT APPLICATION NUMBER: US/08/650,766D
CURRENT PILING DATE: 1996-05-20
EARLIER APPLICATION NUMBER: US 60/012,600
EARLIER FILING DATE: 1996-03-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 1.7e+02;
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                 EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1998-02-22
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 24
LENGTH: 1565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08650766D Patent No. 6015690
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Streptomyces venezuelae
US-09-320-878-24
             EARLIER FILING DATE: 1998-05-06
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Best Local Similarity 93.3%;
Matches 14; Conservative
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Matches 14; Conservative
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US-08-650-766-2
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US-08-650-766-2/c
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Sequence 9, Appli

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                350425 seqs, 194966369 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                           Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
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| Cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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Database

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Result	1t		Query				
ĭ	No.	Score	Match	Match Length DB	DB	ID	Description
Ü	-	13.4	89.3	114	10	US-09-864-761-26040	Sequence 26040, A
	7	13.4	89.3	458	10	US-09-864-761-32413	Sequence 32413, A
	33	13.4	89.3	543	10	US-09-864-761-15909	Sequence 15909, A
υ	4	13.4	89.3	580	10	US-09-864-761-9604	Sequence 9604, Ap
	Ŋ	13.4	89.3	592	10	US-09-864-761-12426	Sequence 12426, A
ပ	9	13.4	89.3	738	10	US-09-759-143-747	Sequence 747, App
ပ	7	13.4	89.3	738	10	US-09-780-669-747	
v	œ	13.4	89.3	738	10	US-09-822-827-747	Sequence 747, App
	σ	13.4	89.3	1458	6	US-09-860-846-9	Sequence 9, Appli
. 1	10	13.4	89.3	1458	10	US-09-861-289-9	Sequence 9, Appli
υ	11	13.4	89.3	2109	10	US-09-815-242-6020	Sequence 6020, Ap
υ	12	13.4	89.3	5828	6	US-09-430-029-1	Sequence 1, Appli
. •	13	13.4	89.3	5881	10	US-09-764-869-2353	Sequence 2353, Ap
U	14	13.4	89.3	9377	10	US-09-801-874-3	Sequence 3, Appli
υ	15	13.4	89.3	13613	0	US-09-860-846-3	Sequence 3, Appli
ပ	16	13.4	89.3	13613	10	US-09-861-289-3	Sequence 3, Appli
	17	13.4	89.3	15016	10	US-09-880-107-3783	Sequence 3783, Ap
	18	13.4	89.3	15857	10	US-09-764-864-1704	Sequence 1704, Ap
. 1	19	13.4	89.3	42450	10	US-09-815-048-3	Sequence 3, Appli

Sequence 258, Appl. 1 Sequence 258, Appl. 1 Sevence 397, App. Sequence 6989, Ap. Sequence 6987, Ap. Sequence 15063, Ap. Sequence 15083, Ap. Sequence 15083, Ap. Sequence 15128, Ap. Sequence 15128, Ap. Sequence 15128, Ap. Sequence 15128, Ap. Sequence 15177, Ap. Sequence 15177, Ap. Sequence 15177, Ap. Sequence 15177, Ap. Sequence 1518, Ap. Sequence 171, Appl. Sequence 171, Appl. Sequence 172, Ap. Sequence 173, Ap. Sequence 174, Ap. Sequence 1	SINGLE EXON NUCLEIC ACID BY MICROARRAY
10 05-09 10 05-09	RESULT 1 US-09-864-761-26040/C US-09-864-761-26040/C Sequence 26040, Application US/09864761 Patent No. US2002004876341 GENERAL INFORMATION: APPLICANT: Penn, Sharid K. APPLICANT: Hanzel, David R. APPLICANT: Hanzel, David R. TITLE OF INVENTION: HUMAN GENOME-DERIVED: TITLE OF INVENTION: GENE EXPRESSION ANALISTIC OF INVENTION: GENE EXPRESSION ANALISTIC OF INVENTION OF GENE EXPRESSION ANALISTIC OF INVENTION OF GENE EXPRESSION ANALISTIC OF INVENTION OF GENE EXPRESSION ANALISTIC OF INVENTION NUMBER: US 60/180,312 PRIOR PELLOATION NUMBER: US 60/180,312 PRIOR PELLOATION NUMBER: US 60/207,456 PRIOR PELLOATION NUMBER: US 60/207,456 PRIOR PELLOATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26 PRIOR PELLOATION NUMBER: US 60/236,359 PRIOR PILING DATE: 2000-10-04 PRIOR PELLOATION NUMBER: PCT/USO1/00666 PRIOR PELLOATION NUMBER: PCT/USO1/00667 PRIOR PELLOATION NUMBER: PCT/USO1/00669 PRIOR PELLOATION NUMBER: PCT/USO1/00669 PRIOR PLING DATE: 2001-01-30 PRIOR PILING DATE: 2001-01-30
45558 45558 1138 11438 11438 1269 2692 2693 360 3869 3869 3869 4447 4457 4467	11.Cation 146763A1 15.00 146763A1 14
27.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.	226040/c 22002000 22002000 22002000 22002000 2200200
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00 000 0 000 0000 0 00 2222222222222222	RESULT 1 Solution 1 Solution 1 Solution 1 Solution 2 Solution 2 Solution 3 Solution 3 Solution 3 Solution 3 Solution 4 Solution 4 Solution 4 Solution 5 Solution 6 Solution 6 Solution 7 Solution 7 Solution 8 Solution 8 Solution 8 Solution 9 Solution

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GAPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GANE EXPRESSION ANALYSIS BY MICROARRY
TITLE OF INVENTION: GANE EXPRESSION ANALYSIS BY MICROARRY
FILE REFERENCE: Aconica-X-1
CURRENT FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-09-37
PRIOR FILING DATE: 2000-09-37
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1

OTHER INFORMATION: NT HIT: gi6671607, EVALUE 2.00e-91

OTHER INFORMATION: SWISSPROT HIT: P97303, EVALUE 1.00e-37

OTHER INFORMATION: EST_HUMAN HIT: BE890758.1, EVALUE 4.30e-01
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Pred. No. 1.7e+02;
); Mismatches 1; Indels
                                          PRIOR PELLICATION NUMBER: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: DCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-0130
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                       APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILING DATE: 2001-01-30
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Best Local Similarity 93.3
Matches 14, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 32413
LENGTH: 458
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Sequence 33413, Application US/09864761

Sequence 33413, Application US/09864761

Sequence 33413, Application US/09864761

SERVICANT Penn, SEATOR SEATOR SEATOR SEATOR SEPTICANT PENN, SEATOR SEATOR
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CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
CTHER INFORMATION: EXTREMAN HIT: BF345368.1, EVALUE 5.00e-31
COTHER INFORMATION: NT HIT: 9111430273, EVALUE 4.00e-31
US-09-864-761-26040
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PRIOR APPLICATION NUMBER: PCT/USO1/00670

PRIOR FILING DATE: 2001-01.30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR APLICATION NUMBER: US 09/774,203

PRIOR APLICATION NUMBER: US 09/774,203

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 26040
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OTHER INFORMATION: MAP TO AC006427.13
OTHER INFORMATION: EXPRESSED IN HEART
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93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFCL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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COTHER INFORMATION: MAP TO ACO06427.13
COTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
COTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
US-09-864-761-9604
              PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 9604
LENGTH: 580
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93.3%; Pred. No. 1.8e+02;
ive 0; Mismatches 1;
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PRIOR PELING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PELING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-01
PRIOR APPLICATION NUMBER: PCT/US01/00670
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PRIOR FILING DATE: 2001-01-30
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Best Local Similarity 93.3
Matches 14; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENNE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION IUMBER: US 60/180,312
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: GS 200-05-26
PRIOR APPLICATION NUMBER: US 60/236,356
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PPLING DATE: 2000-10-04
PRIOR PPLING DATE: 2000-09-27
PRIOR PPLING DATE: 2000-09-27
PRIOR PPLING DATE: 2000-09-27
PRIOR PPLING DATE: 2000-09-27
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                                                                       PRIOR FILING DATE: 2001-01-00
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 15909
LENGTH: 543
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Pred. No. 1.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: MAP TO AL121787.22
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
US-09-864-761-15909
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILLING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                    PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
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PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00661
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.3%;
93.3%;
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Matches 14; Conservative
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US-09-864-761-9604/c
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US-09-822-827-747/C

Sequence 747, Application US/09822827

Sequence 747, Application US/09822827

Sequence 747, Application US/09822827

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: 0S/09/822,827

CURRENT PILLING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOGTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 747

LENGTH: 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hutal, John
APPLICANT: MONELIL, PAIRTICIA D.
APPLICANT: MONELIL, PAIRTICIA D.
APPLICANT: HOUGHTON, REWINDED L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121-477C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.3%; Score 13.4; DB 10; Length 738; 93.3%; Pred. No. 1.8e+02; Live 0; Mismatches 1; Indels 0
          ÷
          Mismatches
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US-09-780-669-747/c
; Sequence 747, Application US/09780669
; Patent No. US20020051977A1
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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OTHER INFORMATION: n=A,T,C or G
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Henderson, Robert A.
Kalos, Michael D.
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Vedvick, Thomas S.
Carter, Darrick
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Hepler, William
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Retter, Marc W.
Stolk, John A.
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Matches 14; Conservative
          Conservative
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                                                                         469 CCTTCTCCCCTGTT 455
                                                   1 CCTICTCGCCCTGIT 15
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li, Samuel
                                                                                                                                                                                                                                             GENERAL INFORMATION:
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          14;
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LENGTH: 738
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APPLICANT:
APPLICANT:
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APPLICANT:
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          Matches
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APPLICANT: Hoplus
TITLE OF INVENTION: William
TITLE OF INVENTION: DAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 747
LUNGTH: 738
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                                                                                                                                                                                                                                                                                               OTHER INFORMATION: MAP TO AL138956.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.92

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.85

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.75
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR RILICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 12426
LENGTH: 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.4; DB 10;
Pred. No. 1.8e+02;
0; Mismatches 1;
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Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICAMT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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; CCATION: (1)...(738)
; OTHER INFORMATION: n=A,T,C or G
US-09-759-143-747
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93.3%;
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Vedvick, Thomas S.
Carter, Darrick
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Retter, Marc W.
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-759-143-747/C
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US-09-864-761-12426
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APPLICANT:
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Gaps

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Sequence 1, Application US/09430029

Batch No. US20020168738A1

GENERAL INFORMATION:

APPLICANT: Yano, Tetsuya; No. US20020168738A1oto, tsuyoshi; Imamura, Takeshi; Can
TITLE OF INVENTION: DNA Fraqment Carrying Toluene Monooxygenase Gene,
TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
TITLE OF INVENTION: Compounds and Aromatic Compounds, and
TITLE OF INVENTION: Compounds and Aromatic Compounds, and
TITLE OF INVENTION: Method for Environmental Remediation
FILE REFERENCE: CF01398208

CURRENT APPLICATION NUMBER: US/09/430,029
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.4; DB 10;
Pred. No. 1.9e+02;
                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE KEFEKENE. ELITARA ULIA.
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR PRICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 6020
LENGTH: 2109
                                                                                                                                                                                                                           ; Sequence 6020, Application US/09815242
; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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93.3%;
                 93.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1492 CCTTCTCGCCCAGTT 1478
                                    14; Conservative
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                                                                             1 CCTTCTCGCCCTGTT 15
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                 Best Local Similarity
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Matches 14; Conserv
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US-09-815-242-6020/c
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US-09-430-029-1/C
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APPLICANT:
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APPLICANT: Lau, Y.

APPLICANT: Abao, I.

TILLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.43840S1

CURRENT APPLICATION NUMBER: US/09/861,289

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 09/105,537

PRIOR FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastsEQ for Windows Version 3.0

LENGTH: 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT PILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
                                                                                                                                                                                                                       Indels
                                                                                                                                                                            Score 13.4; DB 10;
Pred. No. 1.8e+02;
0; Mismatches 1;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09860846 Patent No. US20020164742A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptomyces venezuelae US-09-860-846-9
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Patent No. US20020110897A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Streptomyces venezuelae
                                                                       ; NAME/KEY: misc_feature
; CCATION: (1)...(738)
; CTHER INFORMATION: n=A,T,C or G
US-09-822-827-747
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93.3%;
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Best Local Similarity 93.3%;
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1458
                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-860-846-9
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, ALPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN AMINOTRANSFERASE

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/801,874

CURRENT APPLICATION NUMBER: 8001-03-09

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FAAFFOR

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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
FRIOR APPLICATION NUMBER: 09/105,537
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1999-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 2.1e+02;
0; Mismatches 1;
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Pred. No. 2e+02;
0; Mismatches
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US-09-860-860-846-3/c
Sequence 3, Application US/09860846
; Patent No. US2002016474281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Streptomyces venezuelae US-09-860-846-3
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     4343 CCTTCTCTCTCTGTT 4357
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Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human
US-09-801-874-3
                                                          RESULT 14
US-09-801-874-3/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
LENGTH: 13613
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3
LENGTH: 9377
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
FILE REFERENCE: PC007
CURRENT APPLICATION UNUBER: US/09/764,869
CURRENT APPLICATION UNUBER: US/09/764,869
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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93.3%; Pred. No. 2e+02;
Live 0; Mismatches 1;
                       P1998-310801
CURRENT FILING DATE: 1999-10-29
EARLIER APPLICATION NUMBER: JP F
BARLIER FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                    TYPE: DNA
ORGANISM: Burkholderia cepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 89.3'
Best Local Similarity 93.3'
Matches 14; Conservative
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LOCATION: (463)..(1455)
COTHER INFORMATION: tomL
FEATURE:
NAME/KEY: CDS
LOCATION: (1495)..(1761)
OTHER INFORMATION: tomM
FEATURE:
NAME/KEY: CDS
LOCATION: (1803)..(3350)
OTHER INFORMATION: tomN
FEATURE:
NAME/KEY: CDS
LOCATION: (1803)..(3350)
OTHER INFORMATION: tomO
OTHER INFORMATION: tomO
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NAME/KEY: CDS
LOCATION: (3810)..(4871)
OTHER INFORMATION: tomP
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OTHER INFORMATION: tomQ
                                                                                                                                                                                                             LOCATION: (234)..(443)
OTHER INFORMATION: tomK
FEATURE:
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GORGANISM: Homo sapiens
US-09-764-869-2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-764-869-2353
                                                                              SEQ ID NO 1
                                                                                                                                                                                           NAME/KEY: CDS
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LENGTH: 5881
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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15
1 ccttctcgccctgtt 15
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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EST:* em_estba: em_estlum em_btc:#	gp_est5: em_estfice em_estfor em_estfor em_gss:
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Database :.	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		T48892 yb07a09.rl	BH019102 L2358k.d_	BM273267 if28e01.y	BH019101 L2357k.d_	AV434035 AV434035	BM142008 if25d08.y
SUMMAKIES			ID	•		BH019102	BM273267	BH019101	AV434035	BM142008
			DB	1	14	17	13	17	10	13
			Match Length DB		309	313	505	513	543	551
	ф	Query	Match		100.0	100.0	100.0	100.0	100.0	100.0
			Score		15	15	15	15	15	15
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15 100.0 617 12 BF971415 15 100.0 626 9 AA102111 15 100.0 653 13 B1997613 15 100.0 653 13 B1997613 15 100.0 659 13 B1997613 15 100.0 659 13 B1997613 15 100.0 676 12 BF716197 15 100.0 830 12 BF716197 15 100.0 830 12 BF716197 15 100.0 830 12 BF716197 15 100.0 839 17 AG100084 15 100.0 939 17 BG46898 16 100.0 972 12 BG16617 17 10.0 972 12 BG16617 18 93.3 257 10 BB466985 18 93.3 257 10 BB466985 18 93.3 257 10 BB466985 18 93.3 280 10 BB4687081 18 93.3 280 10 BB4687081 19 93.3 280 10 BB4687081 19 93.3 280 10 BB4687081 19 93.3 302 12 BF89281 19 93.3 302 12 BF89281 19 93.3 370 10 BB4687281 11 93.3 370 10 BB4687281 11 93.3 370 10 BB4687281 14 93.3 370 10 BB4687281 16 93.3 370 10 BB4687281 17 93.3 370 10 BB4687281 18 93.3 370 10 BB4687281 17 93.3 370 10 BB468781 18 93.3 370 10 BB468	L (DASES 1 to 309) S Hillier, L. Lennon, G., Becker, M., Bonall Chissoe, S., Dietrich, N., DuBuque, T., Far, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Multman, M., Farsons, J., Prange, C., J. Schellenberg, K., Soares, M.B., Tan, F., Underwood, K., Wohldmann, P., Waterston, R. Generation and analysis of 280,000 human Genome Res. 6 (9), 807-828 (1996) E. Contact: Wilson RK Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Tel: 314, 286 1800 Fax: 314, 286 1800 Fax: 314, 286 1810 Fax: 314, 286 1810 Fax: 314, 286 1810
15 100 15 100 15 100 15 100 15 100 15 100 15 100 15 100 15 100 16 10 10 10 10 10 10 10 10 10 10 10 10 10	Hill Chis Chis Chis Chode Geno Geno Geno Geno Geno Tel:

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Query Match
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Matches 15; Conservative
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1 (bases 1 to 313)

Myler, P. J., Vogt, C., Cawthra, J., Klacking, M., Marty, A., Mack, J.,
Myler, P. J., Vogt, C., Cawthra, J., Sisk, E., Fazelinia, G., Aggarwal
, G., Nelson, S., Seyler, A., Worthey, E. and Stuart, K.
Leishmania major Friedlin Cosmid End Sequences
Unpublished (2000)
Contact: Myler PJ
Seattle Blomedical Research Institute
4 Nickerson Street, Seattle, WA 98109-1651, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH019102
L2358k.d_HygT3.1 Leishmania major Friedlin Cosmid Genomic Library
Leishmania major genomic clone L2358k, DNA sequence.
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                                                                                                                                                                                                                                                                           /note="Vector: cLHYG; Site_1: BamHI; Genomic DNA from Leishmania major Friedlin was partially digested with Sau3A1, size selected, and ligated with BamHI-digested cLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivens et al., Genomics Research, 8:135-145 (1998). The CLHYG
High qality sequence stops: 239
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RPl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Leishmania major Friedlin Cosmid Genomic Library"
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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0
                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB1491333"
/db_xref="taxon:9606"
/clone="IMAGE:70456"
/clone="lib="Stratagene placenta (#937225)"
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 15; DB 14;
100.0%; Pred. No. 6.1e+03;
iive 0; Mismatches 0;
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/organism="Leishmania major"
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                                                                                            High quality sequence stop: 239.
Location/Qualifiers
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/db_xref="taxon:5664"
/clone="L2358k"
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Fax: 206 284-0313
Email: mylerpiebbri.org
Seq primer: Hyg73
Class: cosmid ends.
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/...c. Sal : Starting library constructed using Site_2: Sal : Starting library constructed using Site_2: Sal : Starting library constructed using SuperScript plasmid Library kit (Life Technologies). CDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; O. F. microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota, Metazoa; Chordates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 505)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Endocrine Pancreas Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA, 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   if28e01.yl Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5677896 5' similar to SW:CAIE_HUMAN P39059 COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1];, mRNA sequence.
vector (Acc. No. CVU59231) is described in Ryan et al, Gene, 131:145-150 (1993)" 2 others
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/db_xref="taxon:9606"
/clone="IMAGE:5677896"
/clone=!ih="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
                                                                                                                                                                                                                                           Gaps
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Other_ESTs: if28e01.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/dev_stage="Adult"
/lab_host="DH10B"
                                                                                                                                                                    Score 15; DB 17;
Pred. No. 6.2e+03;
; Mismatches 0;
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
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                                                                                                                                                                           100.0%;
100.0%;
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and

Saga, N.

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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. .543
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Jackson, Y. and Bowers, Y.,
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Porphyra yezoensis"
/strain="TU-1"
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/clone="PM09706_r"
/clone="PM09706_r"
/clone="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   AV434035 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PM037d06_r 5', mRNA sequence.
AV434035
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Other_ESTs: if25d08.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                             Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 10; Length 543;
Pred. No. 7e+03;
                                                                                                                                                                                                                                    Porphyra.
1 (bases 1 to 543)
Nikaldo,I., Asamizu,E., Nakajima,M., Nakamura,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 g
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                                                                                                                                                                              Porphyra yezoensis
Eukaryota, Rhodophyta;
                                                                                          AV434035.1 GI:8589260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                      Porphyra yezoensis.
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Matches 15; Conservative
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Leishmania.
Leishmania.
1 (bases 1 to 513)
Myler, P.J., Vogt,C., Cawthra,J., Klacking,M., Marty,A., Mack,J.,
Munden,H., Nguyen,D., Robertson,L., Sisk,E., Fazelinia,G., Aggarwal
,G., Nelson,S., Seyler,A., Worthey,E. and Stuart,K.
Leishmania major Friedlin Cosmid End Sequences
Unpublished (2000)
Jungle-stranded (unhybridized) plasmids were isolated hydroxyapatite chromatography and used to make this rear and a second constant of the co
                                                                                                                                                                                                                                          ö
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L2357k.d_HygT3.1 Leishmania major Friedlin Cosmid Genomic Library
Leishmania major genomic clone L2357k, DNA sequence.
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//note="Vector: CLHYG; Site_l: BamHI; Genomic DNA from Leishmania major Friedlin was partially digested with Sau3AI, size selected, and ligated with BamHI-digested CLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivens et al., Genomics Research, 8:135-145 (1998). The CLHYG vector (Acc. No. CVU59231) is described in Ryan et al, Gene. 131:145-150 (1993).
                                                                                                                                                                                                                                       Gaps
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/db_xref="taxon:5664"
/clone="L357k"
/clone="Lba"Leishmania major Friedlin Cosmid Genomic
/clone_lib="Leishmania major Friedlin Cosmid Genomic
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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4 Nickerson Street, Seattle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-0313
                                                                                                                                                                           100.0%; Score 15; DB 13; 100.0%; Pred. No. 6.9e+03;
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/organism="Leishmania major"
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      20. Single-stranded
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Seq primer: Hygr3
Class: cosmid ends.
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BH019101.1 GI:14197807
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1 138 c
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Best Local Similarity 100.
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/note="Organ: Pancreas; Vector: pSPORTI; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT prining. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; O.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized)
Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brownefas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov Seq primer: -40RP from Gibco High quality sequence stopp: 414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
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602272934F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4361024 5',
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NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLAM10003 row: c column: 09

High quality sequence stop: 614.
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/sex="Both"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 617)
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                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Islets of Langerhans"
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                                                                                                                                                                                                                 1. .551
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/lab_host="DH10B"
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BF971415.1 GI:12338630
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148 c
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/clone="IMAGE:4351024"
/clone=lib="NIH_MGC_84"
/tlone=lib="NIH_MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/tlab_host="BH10B (phage-resistant)"
/note="organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr
primed. Average insert size 1.229 kb. Library enriched for plined. Average insert size 1.229 kb. Library enriched for Note: this is a NIH_MGC Library."
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1 (bases 1 to 626)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, S. M. Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Woldman, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
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zk87h09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:489857 3' similar to SW:CAlE_HUMAN P39059 COLLAGEN ALPHA 1(XV
) CHAIN PRECURSOR. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson wustl.edu
Email: est@watson wustl.edu
Email: est@watson wustl.edu
Inscrt Length: 867 Std Error: 0.00
Seq primer: -40Mil3 fwd. from Amersham
High quality sequence stop: 453.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:3804444"
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/lab_host="DH10B"
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Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                 BI997613.1 GI:16432387
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                         252 CCTTCTCGCCCTGTT 238
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                       1 CCTICICGCCCIGIT 15
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                                                                                                                                                                                                                                                                                         zk87h09.rl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone | MAGE:489857 5' similar to SW:CAlE_HUMAN P39059 COLLAGEN ALPHA 1(XV AA099915
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; List strand cDNA was primed with a Not I oliqo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 867 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                   Gaps
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went through one round of normalization. Library constructed by M. Fatima Bonaldo."
179 c 161 g 166 t 4 others
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                                                                                             Length 626;
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/Organism="Homo sapiens"
/Organism="Homo sapiens"
/Ob_xref="GDB:3804444"
/db_xref="taxon:9606"
/clone="IMAGE:489857"
/clone_lib="Soares_pregnant_uterus_NDHPU"
                                                                                                                                 Indels
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                                                                                           100.0%; Score 15; DB 9; I
100.0%; Pred. No. 7.2e+03;
ive 0; Mismatches 0;
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Location/Qualifiers
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/lab_host="DH10B"
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AA099915.1 GI:1646057
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                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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AA099915/c
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/Glone_lib="datu: bason: 1003"
// Lambda Zap II"
// Lambda Zap II"
// Lambda Zap II"
// Note="Vector: pBluescript II SK-; Site_1: ECORI; Site_2: Xhoi; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP + Sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized The CDNA was directionally cloned into lambda
1031050H04.y2 C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                         Lefebvre
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                                                                                                                                                                                                                                                  Chlamydomonas reinhardtii
Ukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 653)
                                                                                                                                                                                                                                                                                                                                                                                   Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebv. P., McDermott, J.P., Shrager, J., Sliflow, C. and Stern, D. Analyses of the Chlamydomonsa reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vascular Plants. Project: 1031
Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: chauser@duke.edu.
Location/Qualifiers
1. 653
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us-09-750-609-9.rst

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/organism="Phytophthora infestans"
/strain="DDR7602, Al mating type"
/db_xref="taxon:4787"
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Best Local Similarity
Matches 15; Conserv
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/clone="IMAGE:316255"
/clone=lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_bost="neuroblastoma"
/lab_host="neuroblastoma"
/lab_host="neuroblastoma
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MY-12-B-02 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.
BE776197
                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Wageningen University
Manenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM122 row: c column: 04
High quality sequence stop: 618.
                                                                                                                                                                          1 (bases 1 to 659)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
Initial assessment of gene diversity for the comycete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
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1. .659
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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   BE313934.1 GI:9134434
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/dow_lib="PlinfestansMy"
/dow_stage="4-week old vegetative, non-sporulating
/dow_stage="4-week old vegetative, non-sporulating
/mycelium in synthetic medium"
/lab_host="8. coli, strain DH5-alpha"
/note="Vector: pSPORTI: Site_1: SalI; Site_2: NotI; Total
RNA was isolated from mycelium of P. infestans DDR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."
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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRLXhoI sites using the following 5;
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF315344 110W-2000 110Ber EST 21-NOV-2000 001902627F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135278 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Autoual institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement. ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

High quality sequence stop: 644.

Inc.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 713)
NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_19"
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BF315344
BF315344.1 GI:11263579
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                                                                                                                                                             BG444893 830 bp mRNA linear EST 15-MAR-2001 GA_Ea0025P19f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0025P19f, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 830)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry, D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
Contact: Wing RA
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/cultivar=8400.
/db_xref="taxon.29729"
/clone="GA_Ea0025919f"
/clone="Ibb="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
/lab_host="E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ609181 839 bp mRNA linear EST 25-JUN BRX 5105 wheat EST endosperm library Triticum aestivum cDNA 5' mRNA sequence. BQ609181 GI:21558520
 Gaps
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/organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clemson University Genomics Institute
Clemson University
100 Oxfadan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 182.
Location/Qualiflers
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BG444893.1 GI:13354545
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1 (bases 1 to 839)
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Conservative
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Matches 15; Conservative
                                  752 CCTTCTCGCCCTGTT 738
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Triticum aestivum
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15;
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AUTHORS Clarke, B., Lambraccht, M. and Rhee, S.

Assessing the utility of Arabidopsis genomic information for interpretary wheat EST sequences

JOURNAL Unpublished (2002)

COMMENT Contact: Lambrecht M

CONTACT: Lambrecht M

Acharication in the Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 3748

Email: Thee@acoma. Stanford.edu.
FEATURES

FLOOR STANDES

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Seg. 108

Chundari

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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December 11, 2002, 13:30:57; Search time 2560.5 Seconds (without alignments) 147.290 Million cell updates/sec 49582208 24791104 seqs, 12571243825 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 US-09-750-609-9 15 1 cctctcgcctgtt 15. Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Title: Perfect score: Sequence: Scoring table: OM nucleic Searched: Run on:

/cgn2_6/ptodata/2/pna/US099C_COMB.seq:* /cgn2_6/ptodata/2/pna/US099D_COMB.seq:* /cgn2_6/ptodata/2/pna/US102A_COMB.seq:* /cgn2_6/ptodata/2/pna/US102B_COMB.seq:* .. Database

1: /cgn2_6/ptodata/2/pna/US6000_COMB.s /cgn2_6/ptodata/2/pna/US6001_COMB.s /cgn2_6/ptodata/2/pna/US6002_COMB.s /cgn2_6/ptodata/2/pna/US6002_COMB.s /cgn2_6/ptodata/2/pna/US6004_COMB.s /cgn2_6/ptodata/2/pna/US6005_COMB.s /cgn2_6/ptodata/2/pna/US6005_COMB.s /cgn2_6/ptodata/2/pna/US6009_COMB.s /cgn2_6/ptodata/2/pna/US6001_COMB.s /cgn2_6/ptodata/2/pna/US6010_COMB.s /cgn2_6/ptodata/2/pna/US6011_COMB.s /cgn2_6/ptodata/2/pna/US6011_COMB.s /cgn2_6/ptodata/2/pna/US6011_COMB.s /cgn2_6/ptodata/2/pna/US6011_COMB.s /cgn2_6/ptodata/2/pna/US6011_COMB.s /cgn2_6/ptodata/2/pna/US6011_COMB.s /cgn2_6/ptodata/2/pna/US6011_COMB.s /cgn2_6/ptodata/2/pna/US6011_COMB.s	/cgn2_6/ptodata/2/pna/US601 /cgn2_6/ptodata/2/pna/US601 /cgn2_6/ptodata/2/pna/US601 /cgn2_6/ptodata/2/pna/US601 /cgn2_6/ptodata/2/pna/US602 /cgn2_6/ptodata/2/pna/US602 /cgn2_6/ptodata/2/pna/US602 /cgn2_6/ptodata/2/pna/US602 /cgn2_6/ptodata/2/pna/US602 /cgn2_6/ptodata/2/pna/US602 /cgn2_6/ptodata/2/pna/US602 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603 /cgn2_6/ptodata/2/pna/US603	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 470, App	Sequence 470, App	Sequence 470, App	Sequence 309, App	Sequence 481, App	Sequence 18784, A	Sequence 2923, Ap	Sequence 4005, Ap	Sequence 4006, Ap	Sequence 4007, Ap	Sequence 4008, Ap	Sequence 7016, Ap	Sequence 7017, Ap	Sequence 7016, Ap	Sequence 7017, Ap	Sequence 99, Appl	Sequence 104, App	Sequence 15, Appl
ID	PCT-US00-35491-9	US-09-750-609-9	US-60-173-682-9	US-09-440-302A-470	US-09-440-302B-470	US-09-440-302-470	US-09-442-366A-309	US-09-698-012-481	US-09-534-856-18784	US-60-230-445-2923	US-09-948-933-4005	US-09-948-933-4006	US-09-948-933-4007	US-09-948-933-4008	US-09-634-306B-7016	US-09-634-306B-7017	US-10-027-632-7016	US-10-027-632-7017	US-60-175-854-99	US-60-175-854-104	PCT-US00-35491-15
DB	1	29	61	18	18	18	18	27	20	67	35	35	35	35	24	24	38	38	61	61	
Length DB	15	15	15	257	257	258	258	472	510	592	601	601	601	601	817	817	817	817	920	920	980
Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
Result No.	П	7	3	4	2	9	7	ထ	о О	10	c 11	c 12	c 13	c 14	c 15	c 16	c 17	c 18	19	20	21

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RESULT 4
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Sequence 9, Application PC/TUS0035491

GENERAL INFORMATION:
APPLICANT: ROBERTSON, DAVId
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: DAVID THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC MODERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC MODERLYING METHODS RELATING THERETO
TITLE OF INVENTION: DAVID MODER: PCT/US00/35491
CURRENT APPLICATION NUMBER: PCT/US00/35491
PRIOR APPLICATION NUMBER: 60/175,456
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/175,456
NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATENTING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
                   Sequence 15, Appli
Sequence 15, Appli
Sequence 16550, A
Sequence 90, Appl
Sequence 90, Appl
Sequence 16300, A
Sequence 16300, A
Sequence 929, Appl
Sequence 926, Appl
Sequence 927, Appl
Sequence 1027, Appli
Sequence 1, Appli
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APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC WITATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: BLOKEN WITATION UNDERLYING METHODS RELATING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27-2-2
CURRENT APPLICATION NUMBER: US/09/750,609
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/175,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Appli
Sequence 1067, Ap
Sequence 1067, Ap
Sequence 18619, A
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100.0%; Pred. No. 1.3e+03;
Live 0; Mismatches 0; Indels
                      9 US-09-750-609-15

2 US-10-213-948-1

1 PCT-0501-10-8631-16550

9 US-09-758-468-90

9 US-10-758-468-90

9 US-10-758-468-90

9 US-10-758-468-90

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10 US-10-211-75-928

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10 US-00-213
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US-09-440-302A-1067
US-09-440-302B-1067
US-60-172-373-18619
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      Best Local Similarity 100
Matches 15; Conservative
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PCT-US00-35491-9
   NUMBER SOFTWARE: Pat
SOFTWARE: Pat
SEQ ID NO.9
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US-09-750-609-9
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Sequence 9, Application US/60173682
Sequence 9, Application David
GENERAL INFORMATION:
APPLICANT: Robertson, David
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIGGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO FILE REFERENCE: Attorney Docket No. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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ilarity 100.0%; Pred. No. 1.6e+03;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.3e+03;
Live 0; Mismatches 0;
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100.0%; Pred. No. 1.3e+03;
ive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Marvey E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CLP11.
CURRENT APPLICATION NUMBER: US/09/440,302A
CURRENT APPLICATION NUMBER: US/09/440,302A
CURRENT APPLICATION NUMBER: US/09/440,302A
FRIOR APPLICATION NUMBER: US/09/053,375
FRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
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PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/173,682
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 15
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ORGANISM: Artificial Sequence
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US-60-173-682-9
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US-09-750-609-9
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Best Local Similarity
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Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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45 CCTTCTCGCCCTGTT 59
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CORGANISM: Homo sapiens
US-09-698-012-481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-698-012-481/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 15; DB 18; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                   APPLICANT: CHASHOW, MATVEY E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11
CURRENT APPLICATION NUMBER: US/09/440,302B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chenchik, Alex
APPLICANT: Likashev, Matvey E.
TILLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11
CURRENT APPLICATION NUMBER: US/09/440,302
CURRENT APPLICATION NUMBER: 09/053,375
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 597
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
LENGTH: 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Nucleic Acid Probe US-09-440-302-470
                                                                                                                                Sequence 470, Application US/09440302B
GRNRRAL INFORMATION: APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
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APPLICANT: Chenchik, Alex
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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1 CCTTCTCGCCCTGTT 15
                  45 CCTTCTCGCCCTGTT 59
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US-09-440-302B-470
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APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuare L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: EXTRACELLULAR MOLECULES
TITLE OF INVENTION: EXTRACELLULAR MOLECULES
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 26334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 481, Application US/09698012
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 15; DB 18;
100.0%; Pred. No. 1.6e+03;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15; DB 27;
Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/698,012;
CURRENT APPLICATION NUMBER: US/09/698,012;
CURRENT FILING DATE: 1900-10-27
PRIOR APPLICATION NUMBER: 60/162,166;
NUMBER OF SEQ ID NOS: 9719-8;
SOFTWARE: FastSEQ for Windows Version 4.0;
LENGTH: 472;
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Array
FILE REFERENCE: CLON-006CIP13
CURRENT APPLICATION NUMBER: US/09/442,366A
CURRENT FILING DATE: 1999-11-17
PRIOR FILING DATE: 1998-033
NUMBER OF SEQ ID NOS: 2216
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 309
LENGTH: 258
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                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic gene fragment US-09-442-366A-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PD-1015 CIP
CURRENT APPLICATION NUMBER: US/09/534,856
CURRENT FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-534-856-18784/c
; Sequence 18784, Application US/09534856
; GENERAL INFORMATION:
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100.0%;
                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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hes 15; Conservative
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
Indels
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ilarity 100.0%; Pred. No. 1.7e+03;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 15; DB 35; 100.0%; Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 6404
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4007
LENGTH: 601
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Best Local Similarity 100.
Matches 15; Conservative
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    Conservative
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                                         1 CCTTCTCGCCCTGTT 15
                                                                27 CCTTCTCGCCCTGTT 13
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Best Local Similarity
Matches 15; Conserv
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US-09-948-933-4007/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Human
US-09-948-933-4007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-948-933-4006
    15;
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      Matches
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GENERAL INFORMATION:
APPLICANT: VEWTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILLE REFERENCE: CLOO0787
CURRENT APPLICATION NUMBER: US/09/948,933
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,399
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 6404
SOUTH OF THE OFFICE OFFI WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00765
CURRENT APPLICATION NUMBER: US/60/230,445
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 3051
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2923
LENGTH: 592
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Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                             Query Match
100.0%; Score 15; DB 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 100.0%; Score 15; DB 67; Best Local Similarity 100.0%; Pred. No. 1.7e+03; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu01124269
                                                                                                                                                                                                   ; OTHER INFORMATION: a, t, c, g, or other US-09-534-856-18784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2923, Application US/60230445 GENERAL INFORMATION:
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                     185 CCTTCTCGCCCTGTT 171
                                                                                                                                                                                                                                                                                                                                              1 CCTTCTCGCCCTGTT 15
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LENGTH: 510
                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                 NAME/KEY: unsure
LOCATION: 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: HUMAN
US-60-230-445-2923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-09-948-933-4005
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Sequence 4007, Application US/09948933
Sequence 4007, Application US/09948933
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AND LIPID DISORDERS, METHODS OF
TITLE OF INVENTION: DEFECTION AND USES THEREOF
FILE REFERENCE: CL000787
CURRENT APPLICATION NUMBER: US/09/948,933
CURRENT FILING DATE: 2001-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                      RESULT 12
US-09-948-933-4006/C
Sequence 4006, Application US/09948933
Sequence 4006, Application US/09948933
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL000787
CURRENT APPLICATION NUMBER: US/09/948,933
CURRENT APPLICATION NUMBER: 60/231,399
PRIOR APPLICATION NUMBER: 60/231,399
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 6404
SOFTWARE: FASTSEQ for Windows Version 4.0
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TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF TITLE OF INVENTION: DFFECTION AND USES THEREOF FILE REFERENCE: CLO00787
CURRENT APPLICATION NUMBER: US/09/948,933
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-08
NUMBER OF SEQ ID NOS: 6404
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 601
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Sequence 7016, Application US/09634306B

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Delymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/09/634,306B

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR PRIOR PLICATION NUMBER: US 60/193,483

PRIOR PLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

PRIOR PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 15; DB 24; Length 817; 100.0%; Pred. No. 1.7e+03; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Human
US-09-948-933-4008
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; ORGANISM: Human
US-09-634-306B-7016
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GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:38:27; Search time 88 Seconds

(without alignments)

122.513 Million cell updates/sec

Title: US-09-750-609-9

Perfect score: 15
Sequence: 1 ccttctcgccctgtt 15
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
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Total number of hits satisfying chosen parameters: 815928

407964 seqs, 359371392 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Pending_Patents_NA_New:*
1: /cgq12_6/ptcdata/1/pna/USO6_NEW_COMB.seq:*
2: /cgq12_6/ptcdata/1/pna/USO6_NEW_COMB.seq:*
3: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*
4: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*
5: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*
6: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*
7: /cgn2_6/ptcdata/1/pna/USO8_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 47407, A	Sequence 47407, A			Sequence 24268, A			2427		24271,			24267,		Sequence 24266, A		1331	Sequence 52, Appl	22,	24,	75,	1036	2, Apr	5	Sequence 4, Appli	4,
ID	US-09-724-676-47407	US-09-724-676A-47407	US-09-724-676-24273	US-09-724-676A-24273	US-09-724-676-24268	US-09-724-676A-24268	US-10-133-937-67	US-09-724-676-24272	US-09-724-676A-24272		US-09-724-676A-24271	US-09-724-676-24267	US-09-724-676A-24267	US-09-724-676-24266	US-09-724-676A-24266	US-10-284-499-14	US-09-513-999C-13316	US-10-271-889-52	US-10-201-365-22	US-10-160-539A-24	US-10-161-493-75	US-10-264-237-1036	US-10-284-499-2	US-10-293-017-5	PCT-US02-32727-4	US-10-057-498-4
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Length	2876	2876	4338	4338	4848	4848	5222	5589	5589	5642	5642	6609	6609	6152	6152	236	352	1458	1565	1565	2177	2520	5128	5132	7430	7430
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US-10-274-994-3 PCT-US02-32727-86 US-10-057-498-86 S-10-271-889-46 S-10-271-889-46 S-10-271-889-46 S-10-271-889-46 S-10-271-889-46 S-10-271-889-46 S-10-271-889-46 S-10-2724-676-32136 S-10-724-676-32136 S-10-724-676-32136 S-10-724-676-24360 S-10-724-676-24360 S-10-724-676-24360 S-10-727-416-9 S-10-271-416-9 S-10-271-416-	IGNMENTS 676 24,676 24,676 ismatches 0; Indel 676A ernative splicing	Score 15; DB 5; Length 2 Pred: No. 51; 0; Mismatches 0; Indels
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88888888888888888888888888888888888888	676-47407 147407, Applica INFORMATION: WAT Compugen LT WAT COMPUSED LT APPLICATION NU FILING DATE: OF SEQ ID NOS: ES PATENTE PATE OF SEQ ID NOS: ES PATENT N VET ES PATENT N VET ES PATENT N VET ES PATENT N VET CCTTCTCGCCCTGTT 15; CONSERVA 15; CONSERVA 15; CONSERVA 15; CONSERVA 16; CONSERVA 17; CONSERVA 18; CONSERVA 19; CONSERVA 11;	2876 A Homo sapie 5A-47407 h Similarity 15; Conserv
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78999999999999999999999999999999999999	RESULT 1 US-09-724-676 Sequence 47 Sequence 47 GENERAL INE TITLE OF 1 TITLE OF 1 FILE REFER CURRENT AF CURRENT AF SOFTWARE: TYPE: DNA CORGANISM: TYPE: DNA CORRENT AF CORRENT	LENGTH: TYPE: DORGANIS
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Squence 67, Application US/10133937

Squence 67, Application US/10133937

Squence 67, Application US/10133937

GENERAL IRFORMATION:
APPLICANT: Ringer, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
TITLE OF INVENTION: DAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
TITLE OF INVENTION: OTHER BIOLOGICAL STATES
FILLE REFRENCE: 11613.560501
CURRENT APPLICATION NUMBER: US/10/133,937
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 99
SSQ ID NO 67
LENGTH: 5222
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                                                                                                                                                                          RESULT 6

Wos-09-724-676A-24268/c

Sequence 24268, Application US/09724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PatentIn version 3.2
                       ;
  Pred. No. 53;
                       Mismatches
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; Sequence 24272, Application US/09724676
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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US-10-133-937-67
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CORGANISM: Homo sapiens
US-09-724-676A-24268
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Best Local Similarity
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US-10-133-937-67/c
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100.0%; Score 15; DB 5; Length 4338;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels
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; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT FILING NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SEQ ID NO 24268
; LENGTH: 4848
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GENERAL INFORMATION:
FAPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENY APPLICATION NUMBER: US/09/724,676A
NUMBER OF SEQ ID NOS: 97222
SOFTWAREN FILING DATE: 2000-11-28
SOFTWARE PATENTIN Version 3.2
SEQ ID NO 24273
LENGTH: 4338
                                                                                                          Sequence 24273, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 4338
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             1422 CCTTCTCGCCCTGTT 1436
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US-09-724-676A-24273/C
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US-09-724-676-24268/c
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Score 15; DB 5; Length 5642; Pred. No. 53; Mismatches 0; Indels (
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SEQ ID NO 24267
LENGTH: 6099
                  APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291814 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24271
LENGTH: 5642
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291814. Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24267
LENGTH: 6099
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Pred. No.
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; Sequence 24267, Application US/09724676
; GENERAL INFORMATION:
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Matches 15; Conservative
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Best Local Similarity 100.
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ORGANISM: Homo sapiens
US-09-724-676A-24267
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US-09-724-676A-24271
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US-09-724-676A-24267/c
    GENERAL INFORMATION:
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Sequence 24272, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNMBER: US/09/724,676A
CURRENT FILNG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN Version 3.2
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Sequence 24271, Application US/09724676
GENERAL INFORMATION:
APPLICAN: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
SOFTWARE: PatentIN version 3.2
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US-09-724-676A-24271/c
; Sequence 24271, Application US/09724676A
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CURRENT FILING DATE: 2000-11-28
              NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24272
LENGTH: 5589
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                          TYPE: DNA
GORGANISM: Homo sapiens
US-09-724-676-24272
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US-09-724-676A-24272
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Best Local Similarity
Matches 15; Conserv
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LENGTH: 5589
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels
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Sequence 24266. Application US/09724676A

GENERAL INFORMATION:
TATLE OF INVENTION VARIABLES OF alternative splicing
TITLE OF INVENTION UNDERS: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SEQ ID NO 24266

LENGTH: 6152
NS-09-724-676-24266/C
Sequence 24266, Application US/09724676
GENERAL INFORMATION
THORMATION:
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24266
LENGTH: 6152
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CORGANISM: Homo sapiens
US-09-724-676A-24266
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CORGANISM: Homo sapiens
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

; Search time 2560 Seconds December 11, 2002, 17:01:38 Run on:

(without alignments) 147.319 Million cell updates/sec

US-09-750-609-9 15 Title:

Perfect score:

1 ccttctcgccctgtt 15 Sequence:

OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

24791104 segs, 12571243825 residues Searched:

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49582208 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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/cgn2_6/ptodata/2/pna/US102B_COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 470, App	Sequence 470, App	Sequence 470, App	Sequence 309, App	Sequence 481, App	Sequence 18784, A	Sequence 2923, Ap	Sequence 4005, Ap	Sequence 4006, Ap	Sequence 4007, Ap	Sequence 4008, Ap	Sequence 7016, Ap	Sequence 7017, Ap	Sequence 7016, Ap	Sequence 7017, Ap	Sequence 99, Appl	Sequence 104, App	Sequence 15, Appl
(I	PCT-US00-35491-9	US-09-150-609-9	US-60-173-682-9	US-09-440-302A-470	US-09-440-302B-470	US-09-440-302-470	US-09-442-366A-309	US-09-698-012-481	US-09-534-856-18784	US-60-230-445-2923	US-09-948-933-4005	US-09-948-933-4006	US-09-948-933-4007	US-09-948-933-4008	US-09-634-306B-7016	US-09-634-306B-7017	US-10-027-632-7016	US-10-027-632-7017	US-60-175-854-99	US-60-175-854-104	PCT-US00-35491-15
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Sequence 17650, A Sequence 17650, A Sequence 213, App Sequence 214, App Sequence 214, App Sequence 212, App Sequence 122, App Sequence 17, App Sequence 17, App Sequence 23575, A Sequence 23755, A Sequence 9375,	Sequence 15275, Apsequence 15275, A Sequence 15275, A Sequence 20101, App Sequence 109, App Sequence 109, App Sequence 29643, A Sequence 9501, App Sequence 65, Appl Sequence 65, Appl Sequence 1550, A Sequence 13501, A Sequence 1	Sequence 17156, A Sequence 17156, A Sequence 17150, A Sequence 13132, A Sequence 13142, A Sequence 5390, Ap Sequence 13447, A Sequence 13447, A Sequence 1351, A Sequence 5521, A Sequence 5521, A Sequence 31850, A Sequence 31850, A Sequence 3149, Ap Sequence 3149, Ap Sequence 3249, Ap	Sequence 31555, A Sequence 31555, A Sequence 4478, Ap Sequence 185, App Sequence 1185, App Sequence 1187, Ap Sequence 7527, Ap Sequence 7527, Ap Sequence 6, Appli Sequence 7527, Ap Sequence 19608, A Sequence 15293, A Sequence 26461, A
US-60-164-320-17650 US-60-183-791-17650 US-08-472-801-213 US-08-668-235-214 US-06-353-987-96987 US-60-353-987-9698 US-08-668-235-213 US-08-668-235-213 US-08-668-235-213 US-09-761-534A-17 US-09-755-374A-13820 US-00-172-360-23755 US-60-172-360-23755 US-60-172-373-9375 US-60-172-373-9375	US-60-278-278-278 US-60-324-185-15275 US-60-197-872-20101 US-08-803-610C-109 US-08-803-610C-109 US-09-803-610C-109 US-09-912-293-556 US-09-612-698-9561 US-09-75-872-65 US-00-605-872-65 US-00-75-872-65 US-00-75-872-65 US-00-75-872-65 US-00-75-872-65 US-00-75-872-65 US-00-73-887-26564 US-00-33-897-26564 US-09-33-897-26564	2 US-09-565-306-73156 1 US-01-182-993-13132 1 US-10-182-993-13132 1 US-10-182-997-913 1 US-10-182-997-913 1 US-10-182-998-5390 2 US-10-203-134-13429 2 US-10-203-135-12444 2 US-10-203-137-13561 2 US-10-203-137-13561 2 US-10-203-139-13011 2 US-10-203-139-13011 2 US-00-236-398-398 6 US-09-270-767-30602 0 US-09-270-767-30602 0 US-09-270-767-30602 0 US-09-329-021-3249 0 US-09-570-849B-13850 0 US-09-570-950-950-950-950-950-950-950-950-950-95	US-60-253-654-31555 US-60-255-592-31555 US-60-478-821-4478 US-60-115-695-80 US-09-880-687-185 US-09-974-300-7193 US-09-974-300-7193 US-09-702-117-6 US-09-702-117-6 US-10-232-992-6 US-10-232-992-6 US-10-232-992-6 US-10-232-997-6 US-09-893-9777 US-09-894-949-8777 US-09-894-949-8777 US-09-894-949-8777 US-09-894-949-8777 US-10-092-399-15-298 US-08-959-395-4735
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Gaps

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Indels

Mismatches Score 15; Pred. No.

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Length 257;

DB 18; 57; ö

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; OTHER INFORMATION: Nucleic Acid Probe US-09-440-302A-470
                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO CURRENT APPLICATION ORDER: 0.2004 0.0. 1242-27-2-2 CURRENT APPLICATION NUMBER: 0.5/09/750,609 CURRENT FILING DATE: 2000-12-28 PRIOR APPLICATION NUMBER: 60/175,456 PRIOR APPLICATION NUMBER: 60/175,456 PRIOR APPLICATION NUMBER: 60/175,682 PRIOR PILING DATE: 1999-12-29 NUMBER: OF SEQ ID NOS: 40 SOFTWARE: Patentin Ver: 2.0 SEQ ID NO 9 LENGTH: 15
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APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REPERBENCE: Attorney Docket No. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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63;
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Sequence 470, Application US/09440302A
Sequence 470, Application US/09440302A
APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
TILLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11
CURRENT APPLICATION NUMBER: US/09/440,302A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
LENGTH: 257
TYPE: DNA
CREATURE: ATLIFICIAL Sequence
FEATURE:
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Pred. No.
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US-60-173-682-9
; Sequence 9, Application US/60173682
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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; ORGANISM: Homo sapiens
US-60-173-682-9
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US-09-750-609-9
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Pred No. 57;
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100.0%; Pred. No. 57;
iive 0; Mismatches 0;
                                                        APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Neurobiology Array
TITLE OF INVENTION: Human Neurobiology Array
CURRENT APPLICATION NUMBER: US/09/440,302B
CURRENT PILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
LENGTH: 257
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GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006C1P11
CURRENT APPLICATION NUMBER: US/09/440,302
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 597
SEQ ID NO 470
LENGTH: 258
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US-09-440-302B-470; Sequence 470, Application US/09440302B; GENERAL INFORMATION:
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100.0%; Pr
tive 0;
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Best Local Similarity 100.
Matches 15; Conservative
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Sequence 4005.
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
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                     FILE REFERENCE: DP-1015 CIP
CURRENT APPLICATION NUMBER: US/09/534,856
CURRENT FILING DATE: 2000-03-24
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 26334
SEG ID NO 18'84
LENGTH: 510
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Best Local Similarity 100.0%; Score 15; DB 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 56;
iive 0; Mismatches
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OTHER INFORMATION: Incyte ID No: hu01124269
TITLE OF INVENTION: EXTRACELLULAR MOLECULES
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COCATION: 488

COTHER INFORMATION: a, t, c, g, or other

US-09-534-856-18784
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-948-933-4005/c
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; ORGANISM: HUMAN
US-60-230-445-2923
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LENGTH: 592
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING STRUCTURAL, SECRETED, AND
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TELEMENT: Gearing, David P.
TITLE OF INVENTION: HOYEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2002-001;
CURRENT APPLICATION NUMBER: US/09/698,012
CURRENT FILING DATE: 2000-10-27
PRIOR PAPLICATION NUMBER: 60,162,166
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 9719
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 258;
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100.0%; Pred. No. 57;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                           APPLICANT: LUKASHEV, MATVEY E.
TITLE OF INVENTION: Human Array
FILE REFERENCE: CLON-006CIP13
CURRENT APPLICATION NUMBER: US/09/442,366A
CURRENT FILING DATE: 1999-11-17
PRIOR PRIOR PRILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 2216
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic gene fragment US-09-442-366A-309.
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                                                                                                                            Sequence 309, Application US/09442366A GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
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Delegeane, Angelo M.
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Stuve, Laura L.
Mullahy, Sara J.
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-698-012-481
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Best Local Similarity
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                                                                                              US-09-442-366A-309
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LENGTH: 472
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APPLICANT:
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GENERAL INFORMATION:

APPLICAME: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLO00787

CURRENT APPLICATION NUMBER: US/09/948,933

CURRENT FILING DATE: 2001-09-10

PRIOR FILING DATE: 2001-09-10

PRIOR FILING DATE: 2001-09-08

NUMBER OF SEQ ID NOS: 6404

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4008
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GENERAL INFORMATION:
APPLICATION:
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APPLICATION UNMER:
CURRENT FILING DATE: 2002-02-1
FRICA REPERENCE: 108027/129
CURRENT FILING DATE: 2002-02-21
FRICA REPELICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2000-07-12
FRIOR PELICATION NUMBER: US 60/218,006
FRIOR PELICATION NUMBER: US 60/193,483
FRIOR PELICATION NUMBER: US 60/193,483
FRIOR PELICATION NUMBER: US 60/193,483
FRIOR PELING DATE: 2000-03-29
FRIOR PELING DATE: 2000-03-29
FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-09-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR PELING DATE: 1999-08-08
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Pred. No. 56;
Mismatches 0; Indels
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100.0%; Pred. No. 55;
ive 0; Mismatches 0;
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Job time: 2589 secs
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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US-09-634-306B-7016/c
       US-09-948-933-4008/c
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US-09-634-306B-7016
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APPLICANT: VENTER:
ASSOCIATED
APPLICANT: VENTER:
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ASSOCIATION OF VENTER:
APPLICANT: VENTER:
ASSOCIATION OF VENTER
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER.
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF FILE REPERENCE: CLOOO787
CURRENT APPLICATION NUMBER: US/09/948,933
CURRENT APPLICATION NUMBER: 60/231,399
PRIOR FILING DATE: 2000-09-08
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100.0%; Pred. No. 56;
ive 0; Mismatches 0;
                                                                                                              Score 15; DB 35;
Pred. No. 56;
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Pred. No. 56;
); Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4007
LENGTH: 601
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100.0%;
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Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
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US-10-165-353A-191 US-10-240-425-15 US-10-266-131-2148 US-09-724-676-40442 US-09-724-676A-40442	US-10-194-163-376 US-09-724-676-38721	US-09-724-676A-3872	US-09-724-676A-42133	PCT-US02-34777-1656	US-10-240-425-947	US-09-724-676-6682	US-09-724-676A-6682	US-09-724-676A-11024	US-10-152-319A-1351	US-09-724-676-40437	US-09-724-676A-4043, US-10-255-536-235	US-10-203-138A-6731	US-10-203-138A-8954	US-10-132-319A-220 US-09-724-676-6671	US-09-724-676-6673	US-09-724-676A-6671	US-US-124-6/6A-66/3 US-10-285-032-23	US-09-724-676-6639	US-09-724-676A-6639	US-09-724-676-6657	US-09-724-676-39073	US-09-724-676A-39073	US-09-724-676-6670.	US-09-724-6764-6670 US-09-724-676-6663	US-09-724-676A-6663	US-09-724-676-28472	US-09-724-676A-28472	US-09-724-676-6681	US-10-145-087A-189	US-10-143-031A-189	US-10-145-092A-189	US-10-165-038A-189	US-10-165-353-189	US-10-172-039A-189	US-10-145-016A-189	US-10-145-129A-189	US-10-165-353A-189	US-09-724-676-28476	US-10-264-237-731	US-09-724-676-6677	US-09-724-676-6679	US-U9-724-676A-6679	US-09-724-676-21190	US-09-724-676A-21190	US-10-240-425-466	US-U9-/24-6/5-6656 US-09-724-676A-6656	US-09-724-676-6684	US-09-724-676A-6684	US-09-724-676-6622	US-U9-/24-6/6A-6622 ITS-09-513-66907-759	US-09-213-999C-729 US-09-724-676-6638
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100.0%; Score 15; DB 5; Length 4338; 100.0%; Pred. No. 1.7;
100.0%; Score 15; DB 5; Length 2876; 100.0%; Pred. No. 1.7;
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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                      RESULT 3
US-09-724-676-24273/C
; Sequence 24273, Application US/09724676
; GENERAL INPORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PATENTIN PERSION 3.2
; SEQ ID NO 24273
: LENGTH: 4338
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US-09-724 676A-24273/C
US-09-724 676A-24273/C
Sequence 24273, Application US/09724676A
GENERAL INFORMATION:
TAPLICART: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT FAPLICATION NUMBER: US/09/724,676A
CURRENT FILIKO DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24273
LENGTH: 4338
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GENERAL INFORMATION:
APPLICANY: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24268
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Best Local Similarity 100.
Matches 15; Conservative
            Best Local Similarity 100.
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CORGANISM: Homo sapiens
US-09-724-676A-24273
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US-09-724-676-24268/c
  Query Match
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SGREAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INFORMATION UNBER: US/09/724,676
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILION DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin Version 3.2
SEQ ID NO 47407
LENGTH: 2876
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; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE COMPUGENT COMPUGEN
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILION DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
; SEQ ID NO 47407
; LENGTH: 2876
; TYPE: DNA
CORRANSM: Homo sapiens
US-09-724-676A-47407
                                        US-09-724-676-6612
US-09-724-676-6614
US-09-724-676-6612
US-09-724-676-6614
US-09-724-676-6610
US-09-724-676-6610
US-09-724-676-6631
US-09-724-676-6631
US-09-724-676-6631
US-09-724-6768-6631
US-09-724-6768-6631
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US-09-724-6768-6631
US-09-724-676-6625
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US-09-724-676-6635
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US-09-724-676A-72
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-724-676A-47407
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US-09-724-676-47407
    TYPE: DNA
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100.0%; Score 15; DB 5; Length 5589; 100.0%; Pred. No. 1.7;
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US-09-724-676A-24272/C
Sequence 24272, Application US/09724676A
SEQUENCE 24272, Application US/09724676A
SEQUENCE 21272, Application US/09724676A
STITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin Version 3.2
SEQ ID NO 24272
LENGTH: 5589
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SEQ ID NO 24271
LENGTH: 5642
Sequence 24272, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24272
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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ORGANISM: Homo sapiens
US-09-724-676A-24272
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ORGANISM: Homo sapiens
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Matches 15; Conserv
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US-09-724-676-24271/c
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APPLICANT: Khan, Javed
APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Peterson, Carsten
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
FILE REPRENCE: 11613 560501
CURRENT-APPLICATION NUMBER: US/10/133,937
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PATENTIN VERSION 3.1
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Query Match

100.0%; Score 15; DB 5; Length 4848;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 15; Conservative 0; Mismatches 0; Indels
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US-09-724-676A-24268/C

Sequence 24268, Application US/09724676A

GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
FITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PATENTIN VERSION 3.2

SOFTWARE: PATENTIN VERSION 3.2
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ive 0; Mismatches 0.
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Best Local Similarity 100.
Matches 15; Conservative
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                                          ; ORGANISM: Homo sapiens US-09-724-676-24268
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US-09-724-676-24272/C
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    LENGTH: 4848
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LENGTH: 5222
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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels
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                       Indels
                                                                                                                                                             RESULT 14
US-09-724-676-24266/C
Sequence 24266, Application US/09724676
GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
FITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DAFTE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24266, Application US/09724676A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INFORMATION:
FILE REFERENCE: 129181.4 Compugen
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24266
LENGTH: 6152
                     0;
    Pred. No. 1.7;
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100.08;
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  Best Local Similarity 100.
Matches 15; Conservative
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                                                              1 CCTTCTCGCCCTGTT 15
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: LENGTH: 6152
: TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24266
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US-09-724-676A-24266/c
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GENERAL INFORMATION:
FAPLICANT: Compugen LTD
TITLE OF INFORMION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT FAPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin Version 3.2
LENGTH: 6099
                                                                         US-09-724-676A-24271/c

Sequence 24771, Application US/09724676A

GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

LENGTH: 5642
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 12918-14 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24267
LENGTH: 6099
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US-09-724-676A-24271
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US-09-724-676A-24267/c
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 10, Appl Sequence 10, Appl	Sequence 10, Appl Sequence 5, Appli	Sequence 6, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 6, Appli	Seguence 2932, Ap	Sequence 2932, Ap		0	7 Sequence 2907, Ap	3 Sequence 4668, Ap	Sequence 2311, Ap	5084 Sequence 106084,		Sequence 8529, Ap	Sequence 3885, Ap	
SUMMARIES	PCT-US00-35491-10 US-09-750-609-10	US-60-173-682-10 PCT-US00-35491-5	PCT-US00-35491-6	03 03 / 30 CO	US-60-173-682-5	us-60-173-682-6	US-09-306-349-2932	US-09-960-481-2932	US-09-076-667-2907	US-09-540-229-47840	US-60-048-002-2907	US-09-637-890-4668	US-09-652-918-2311	US-09-865-439A-106084	US-60-207-458-150004	US-09-552-086-8529	US-07-952-911-3885	US-09-293-972-23661
DB	1 29	1	1	2 5	61	61	17	36	14	21	48	24	25	33	64	22	3	16
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US-60-173-682-10
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Sequence 10, Application PC/TUS0035491
GENERAL INFORMATION:
APPLICANT: Robertson, David
APPLICANT: Blakely, Randy D.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
CURRENT APPLICATION NUMBER: PCT/V300/35491
SCHRENT FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PARLETIN Ver. 2.0
Sequence 23661, A Sequence 8098, Ap Sequence 11236, A Sequence 11236, A Sequence 2488, Ap Sequence 2079, Ap Sequence 13056, A Sequence 9898, Ap Sequence 10936, A Sequence 10936, A Sequence 15997, A Sequence 55997, A Sequence 559
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APPLICANT: Blakely, Randy D.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPECTIC METHODS RELATING THERETO FILE REFERENCE: Attorney Docket No. 1242-27-2-2
CURRENT APPLICATION NUMBER: US/09/750,609
PRIOR APPLICATION NUMBER: 60/175,456
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Sequence 998, App
Sequence 184, App
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Best Local Similarity 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels
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US-09-565-240-8098
US-09-465-877-11236
US-09-906-555-11236
US-09-804-730-2488
US-09-652-918-2079
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US-09-906-555-13056
US-09-785-276A-9898
US-09-786-276A-9898
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US-09-654-617-15997
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US-09-652-918-998
US-09-663-784-184
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                      1 CCTTCTCCCCTGTT 15
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ORGANISM: Homo sapiens
PCT-US00-35491-10
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US-09-750-609-10
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PET-USOUS 5, Application PC/TUS0035491

SQUENCE 5, Application PC/TUS0035491

GENERAL INFORMATION:

APPLICANT: Robertson, David

TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO FILE REFERENCE: Attorney Docket No. 1242-27 PCT

CURRENT FILING DATE: 2000-12-28

PRIOR PILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: 60/175,456

PRIOR FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATENTING VAR: 2.0
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APPLICANT: Robertson, David
APPLICANT: Robertson, David
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 15; DB 61; 100.0%; Pred. No. 2.6e+03;
                                                                                                                                                                                                                                               100.0%; Score 15; DB 29;
100.0%; Pred. No. 2.6e+03;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB 1;
Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION WUMBER: 60/173,682
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 10
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 10, Application US/60173682; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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CORGANISM: Homo sapiens
PCT-US00-35491-5
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CRGANISM: Homo sapiens
US-60-173-682-10
                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-750-609-10
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Sequence 6, Application US/09750609

GENERAL INFORMATION:
APPLICANT: Robertson, David
APPLICANT: BLAKely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REPERENCE: Attorney Docket No. 1242-27-22
CURRENT APPLICATION NUMBER: US/09/750,609
CURRENT APPLICATION NUMBER: 60/175,456
PRIOR APPLICATION NUMBER: 60/175,456
PRIOR APPLICATION NUMBER: 60/175,456
PRIOR FILING DATE: 2000-01-1
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 6
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROBERTSON, David
APPLICANT: BLAKELY, Randy D.
APPLICANT: BLAKELY, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REFERENCE: ALTORING DOCKET NO. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO S.
ELENGTH: 41
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GENERAL INFORMATION:
APPLICANT: Robertson, David
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPBUTIC METHODS RELATING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 41
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US-60-173-682-5
; Sequence 5, Application US/60173682
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15, Conservative
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CORGANISM: Homo sapiens
US-60-173-682-5
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US-60-173-682-6/c
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Sequence 6, Application FC/TUS0035491

Sequence 6, Application FC/TUS0035491

GENERAL INFORMATION:

APPLICANT: Blakely, Bandy D.

TITLE OF INVENTION: DIAGNOSTIC AND 1242-27 PCT

TITLE OF INVENTION: DIAGNOSTIC AND 1242-27 PCT

CURRENT FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: 60/175,456

PRIOR FILING DATE: 2000-01-11

PRIOR PRILICATION NUMBER: 60/173,682

PRIOR FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATENTIN VET: 2.0
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100.0%; Pred. No. 3e+03;
ive 0; Mismatches 0;
      Mismatches
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Best Local Similarity 100.
Matches 15; Conservative
      Conservative
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Best Local Similarity
Matches 15; Conserv
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US-09-750-609-6/c
      15;
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LENGTH: 41
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APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Inggrid E.
APPLICANT: Maufhon, Rebecca E.
APPLICANT: Maufhon, Rebecca E.
APPLICANT: Klingler, TO M.
TITLE OF INVENTION: HUMAN BRAIN
MINMER OF SEQUENCES: 44483
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 15; DB 14; 100.0%; Pred. No. 3.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCHEST LATER INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0370P
TELECOMMUNICATION INFORMATION:
TELEFENDE: (415) 85-055
TELEFRAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 2907:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 47840, Application US/09540229
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Mullahy, Sara J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 6.1 for Wi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,667
FILLING DATE:
                                                                                                                                        Sequence 2907, Application US/09076667 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                             Gooding, Douglas H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 248 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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1 CCTTCTCCCCCTGTT 15
                       3 CCTTCTCCCCCTGTT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: 3268389H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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US-09-540-229-47840
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MOLECULE TYPE:
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                                                                                                     RESULT 12
US-09-076-667-2907
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                      APPLICANT:
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GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Byrum, Joseph R.

APPLICANT: Byrum, Joseph R.

TITLE OF INVENTION: UNDER: J.

TITLE OF INVENTION: UNDER: J.

FILE REFERENCE: 38-21(15367)C

CURRENT APPLICATION NUMBER: US 09/306,481

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: US 09/306,349

PRIOR APPLICATION NUMBER: US 09/306,349

SEQ ID NO 2932

SEQ ID NO 2932

LENGTH: 197
                                                                                                                                                                                                                                                                                     Sequence 2932, Application US/09306349
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: NUCLE: Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: NUCLE: COURENT POPLICANT: 1367)B
CURRENT APPLICANTON MUMBER: US/09/306,349
CURRENT FILING DATE: 1999-05-07
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100.0%; Score 15; DB 36; Length 197;

Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                   Length 41;
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Best Local Similarity 100.0%; Score 15; DB 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 0;
                                                                 100.0%; Score 15; DB 61; 100.0%; Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COTION: (1)..(197)
OTHER INFORMATION: Unsure at all n locations
THER INFORMATION: Clone ID: 701040886H1
US-09-960-481-2932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: unsure at all n locations; OTHER INFORMATION: Clone ID: 701040886H1 US-09-306-349-2932
                                                                                                          Mismatches
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                                                                   Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                          28 CCTTCTCCCCTGTT 14
  ; ORGANISM: Homo sapiens
US-60-173-682-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Glycine max
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LENGTH: 197
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Gaps

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Query Match
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APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS
FILE REFERENCE: PD-1033 CIP
CURRENT APPLICATION NUMBER: US/09/540,229
CURRENT FILING DATE: 2000-03-31
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEC ID NOS: 193582
SOFTWARE: PERL Program
SEC ID NO 47840
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Nalngler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: HUMAN BRAIN NUMBER OF SEQUENCES: 4483
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/048,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 15; DB 21; Best Local Similarity 100.0%; Pred. No. 3.7e+03; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00535318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0370P
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 845-0555
TELEFAN: (415) 845-4166
INFORMATION FOR SEQ ID NO: 2907:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
CATION: 211
S CTHER INFORMATION: a, t, c, g, or other
US-09-540-229-47840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2907, Application US/60048002 GENERAL INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCTTCTCCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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GENERAL INFORMATION:
APPLICANT: Shjan, Andrew W.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Galvin, Katherine
APPLICANT: Culpepper, Janice A.
APPLICANT: Culpepper, Janice A.
APPLICANT: Leiby, Kevin R.
APPLICANT: Vasicek, Tom
APPLICANT: Vasicek, Tom
APPLICANT: Villeval, Jean-Luc M. G.
APPLICANT: Villeval, Jean-Luc M. G.
APPLICANT: Wingsbury, Gillian A.
APPLICANT: Tringsbury, Gillian A.
APPLICANT: Wingsbury, Gillian A.
APPLICANT: Wingsbury, Gillian A.
APPLICANT: Goldon, 152-001
CURRENT APPLICATION NUMBER: US/09/637,890
CURRENT APPLICATION NUMBER: GO/147,939
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4668
LENGTH. 227
                                                                                                                                Ouery Match
100.0%; Score 15; DB 48; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels (
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100.0%; Pred. No. 3.8e+03;
iive 0; Mismatches 0;
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Job time: 2561.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4668, Application US/09637890
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Shyjan, Andrew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
hes 15; Conservative
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; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 3268389H1
US-60-048-002-2907
                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-637-890-4668/c
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(without alignments)
122.513 Million cell updates/sec
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| (9qn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
| (9qn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
| (9qn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
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| (9qn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
| (9qn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
| (9qn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*)
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                          2002, 13:38:27
                                                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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15
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Sequence 13316, A Sequence 1036, Ap Sequence 1245, Ap Sequence 28339, A Sequence 24274, A Sequence 2247, Ap Sequence 2234, Ap Sequence 2234, Ap Sequence 2231, Ap Sequence 2246, Ap Sequence 2246, Ap Sequence 2246, Ap Sequence 2246, Ap Sequence 2245, Ap Sequence 2227, Ap Sequence 2237, Ap Sequence 2233, Ap Description US-09-620-607B-1245 US-09-724-676-38339 US-09-724-676-24274 US-09-724-676-24274 US-09-724-676-2247 US-09-724-676-2247 US-09-724-676-2247 US-09-724-676-2234 US-09-724-676-2231 US-09-724-676-2231 US-09-724-676-2231 US-09-724-676-2221 US-09-724-676-2221 US-09-724-676-2221 US-09-513-999C-13316 US-09-724-676A-2240 US-09-724-676-2246 -09-724-676A-2246 -09-724-676-2245 6A-2245 US-09-724-676A-2233 US-09-724-676-2220 '6A-2214 -1036SUMMARIES Ω DB 1030 11509 11509 11509 11712 11712 11755 11825 11825 Length Query Score Result Š. O

Sequence 2220, Ap Sequence 2232, Ap Sequence 2239, Ap Sequence 2239, Ap Sequence 2251, Ap Sequence 2251, Ap Sequence 2218, Ap Sequence 2218, Ap Sequence 2218, Ap Sequence 2218, Ap Sequence 2226, Ap Sequence 2226, Ap Sequence 2226, Ap Sequence 2226, Ap Sequence 2226, Ap Sequence 2213, Ap Sequence 2213, Ap Sequence 2213, Ap Sequence 2213, Ap	ded Human Proteins.	Length 352; ; Indels 0; Gaps 0; Antibodies
3 2028 5 US-09-724-676A-2220 3 2029 5 US-09-724-676-2232 3 2021 5 US-09-724-676A-2232 3 2071 5 US-09-724-676A-2239 3 2072 5 US-09-724-676A-2239 3 2072 5 US-09-724-676-2239 3 2072 5 US-09-724-676A-2239 3 2074 5 US-09-724-676A-2218 3 2074 5 US-09-724-676A-2218 3 2117 5 US-09-724-676A-2238 3 2229 5 US-09-724-676A-2238 3 2229 5 US-09-724-676A-2238 3 2274 5 US-09-724-676A-2213 3 2275 5 US-09-724-676A-2213	ALIGNMENTS  6/c  typlication US/09513999C  ert, A.  ert, A.  dano, J.Y.  Clano, J.Y.  Clano, J.Y.  Clano, J.Y.  Clano, J.Y.  NOW NUMBER: US/09/513,999C  ATE: 2000-02-24  NN NUMBER: US 60/122,487  FE: 1999-02-26  NOS: 36681  C. pm  feature  feature  CON: k-g or t  feature  feature  for in the continuation of the continuation	; Score 15; DB 5; ; Pred. No. 1e+02; 0; Mismatches 0 10264237 cids, Proteins, and 5/10/264,237 -04 vusol/16450
C 28 C 29 C 29 C 31 C 31 C 31 C 32 C 33 C 34 C 34 C 34 C 34 C 34 C 34 C 34	RESULT 1  US-09-513-999C-13316/c  Sequence 13316, Application US/09) GERRAL INFORMATION: APPLICANT: Dumas Milne Edwards, APPLICANT: OURENT STREET S	Query Match Best Local Similarity 100.08 Matches 15; Conservative Qy 1 CCTTCTCCCCCTGTT 15 Db 149 CCTTCTCCCCTGTT 135 RESULT 2 US-10-264-237-1036 Sequence 1036, Application US/; GENERAL INFORMATION: APPLICANT: BIRSE et al. TITLE OF INVENTION: Nucleic APPLICANTS PRICATION NUMBER: US FILE REFERENCE: PAINTPER: US CURRENT FILING DATE: 2002-10 PRIOR FILING DATE: 2002-10 PRIOR FILING DATE: 2010-105-18

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Gaps

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Indels
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Variants of alternative splicing TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SOFTWARE: Patentin version 3.2 LENGTH: 1030
                                                                                                                                                                                                        APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291814 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 38339
LENGTH: 908
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100.0%; Pred. No. 3.4e+02;
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100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0;
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  Mismatches
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                                                                                                                                                                        Sequence 38339, Application US/09724676A GENERAL INFORMATION:
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Best Local Similarity 100.
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CORGANISM: Homo sapiens
US-09-724-676-24274
                                        1 CCTTCTCCCCTGT 14
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ORGANISM: Homo sapiens
US-09-724-676A-38339
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Best Local Similarity
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US-09-724-676A-24274/C
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US-09-724-676-24274/c
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US-09-724-676A-38339
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LENGTH: 1030
TYPE: DNA
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nehls, Michael
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Mutated Mammalian Cells and
TITLE OF INVENTION: Novel Mutated Mammalian Cells and
TITLE OF INVENTION: Novel Mutated Mammalian Cells and
TITLE OF INVENTION: NOVEL MAINAIS
FILE REFERENCE: LEX-003-USA
CURRENT FAPLICATION NUMBER: US 60/144942
PRIOR APPLICATION NUMBER: US 60/144942
PRIOR APPLICATION NUMBER: 1999-07-20
NUMBER OF SEQ ID NOS: 1848
SOFTWARE: FREESEQ for Windows Version 4.0
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Sequence 38339, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT FLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 38339
LENGTH: 908
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0;
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3.2e+02;
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Pred. No.
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        PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1036
LENGTH: 2520
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100.0%; Pre
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Best Local Similarity 100.
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-09-724-676-38339
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CORGANISM: Mus musculus
US-09-620-607B-1245
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Best Local Similarity
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                   SOFTWARE: Patentin version 3.2
SEQ ID NO 2234
LENGTH: 1667
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Matches 14; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-724-676-2221
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US-09-724-676A-2234/c
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     NUMBER OF SEQ ID
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LENGTH: 1667
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PALENTIN VERSION 3.2
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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GENERAL INRORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
                                                   Score 14; DB 5; Le
Pred. No. 3.4e+02;
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Matches 14; Conservative 0
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Best Local Similarity 100.
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; ORGANISM: Homo sapiens
US-09-724-676A-24274
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US-09-724-676A-2247
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US-09-724-676A-2247/c
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US-09-724-676-2247/c
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LENGTH: 1509
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LENGTH: 1509
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 2221
LENGTH: 1712
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TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
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Search completed: December 11, 2002, 16:59:27 Job time: 89 secs

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93.3%; Score 14; DB 5; Length 171
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE CAMPUT COMPUGEN LTD
TITLE REFERENCE: 129181.4 Compugen
CURRENY APPLICATION NUMBER: US/09/724,676
CURRENY FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE Patentin version 3.2
SEQ ID NO 2240
LENGTH: 1755
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 2240
LENGTH: 1755
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REPRENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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Best Local Similarity 100.
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-09-724-676-2240
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ORGANISM: Homo sapiens
US-09-724-676A-2221
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US-09-724-676A-2240/c
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US-09-724-676-2240/c
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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. 1	2 15	100.0	15	29	US-09-750-609-10	Sequence 10, Appl
1	3 15	100.0	15	61	US-60-173-682-10	Sequence 10, Appl
7	1 15	100.0	41	Н	PCT-US00-35491-5	Sequence 5, Appli
ט	5 15	100.0	41	-	PCT-US00-35491-6	
v	5 15	100.0	41	29	US-09-750-609-5	Sequence 5, Appli
Ü	7 15	100.0	41	53	us-09-750-609-6	Sequence 6, Appli
w	3 15	100.0	41	61	US-60-173-682-5	Sequence 5, Appli
υ	9 15	100.0	41	61	US-60-173-682-6	Sequence 6, Appli
ĭ	15	100.0	197	17	US-09-306-349-2932	Sequence 2932, Ap
11	1 15	100.0	197	36	US-09-960-481-2932	Sequence 2932, Ap
17	2 15	100.0	248	14	US-09-076-667-2907	Sequence 2907, Ap
33	3 15	100.0	248	21	US-09-540-229-47840	Sequence 47840, A
14	1 15	100.0	248	48	US-60-048-002-2907	Sequence 2907, Ap
C 15	5 15	100.0	327	24	US-09-637-890-4668	Seguence 4668, Ap
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c 15	3 15	100.0	376	22	US-09-552-086-8529	Sequence 8529, Ap
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425 23 US 09-606-977-29398 Sequence 2339, 427 11 US 09-606-977-4986 Sequence 2330, 427 12 US 09-506-920-623-6230 Sequence 2323, 428 17 US 09-501-602-2033 Sequence 2323, 429 17 US 09-91-60-2033 Sequence 1384, 429 17 US 09-91-60-2033 Sequence 1384, 429 17 US 09-91-60-2033 Sequence 1384, 429 17 US 09-91-60-91-91-91-91-91-91-91-91-91-91-91-91-91-	47 30 US-00-144-004-2070 Sequence 28308,
25 10.5.09-606-977-29398 sequence 23399, 271 10.5.09-606-977-29398 sequence 23022, 271 10.5.09-606-2924-2522 sequence 23022, 271 10.5.09-606-2924-2522 sequence 23026, 271 10.5.09-306-2924-2023 sequence 23026, 271 10.5.09-306-2924-2023 sequence 23026, 272 10.5.09-406-2924-2023 sequence 23026, 272 10.5.09-406-2924-2923 sequence 23026, 272 10.5.09-306-2924-2923 sequence 23026, 272 10.5.09-306-292-2923 sequence 23026, 272 10.5.09-306-292-392-3923 sequence 23026, 272 10.5.09-306-292-392-392-392-392-392-392-392-392-392	5.7 448 23 US-09-619-643-28308 Sequence 28308,
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Sequence 186246, Sequence 186246, Sequence 8577, Ap Sequence 8572, Ap Sequence 8552, Ap Sequence 7501, Ap Sequence 7501, Ap Sequence 7312, Ap Sequence 2316, Ap Sequence 2316, Ap Sequence 2316, Ap Sequence 3392, Ap Sequence 3393, A Sequence 340983, Sequence 420983, Sequence 375, App Sequence 13933, Sequence 101501, Sequence 119338, Sequence 119338, Sequence 119338, Sequence 119338, Sequence 119338, Sequence 1145421, Sequence 1145421, Sequence 11453, A Sequence 24312, A Sequence 94312, A Sequence 24312, A Sequence 94312, A Sequence 94312, A Sequence 24412, A Sequence 94312, A Sequence 94312, A	OSTATIC INTOLERANCE AND DS RELATING THERETO	Length 15; Indels 0; Gaps 0;
US-10-235-926-2527 US-09-654-617-186246 US-10-029-386-8577 US-09-71-197-8552 US-08-971-197-8552 US-08-971-197-8552 US-08-971-197-8552 US-09-724-750-7501 US-60-171-431-7501 US-60-171-431-7501 US-60-171-431-7501 US-60-171-431-7501 US-60-196-710-3392 US-09-654-617-420983 US-09-654-617-420983 US-09-654-617-420983 US-09-654-617-420983 US-09-654-617-420983 US-09-654-617-420983 US-09-654-617-420983 US-09-654-617-420983 US-09-654-617-420983 US-09-654-617-420983 US-09-634-3068-13938 US-09-813-13484 US-00-207-458-145421 US-00-207-458-145421 US-09-538-524-94312 US-09-933-524-94312 US-09-933-524-94312 US-09-933-524-94312 US-09-933-524-94312 US-09-933-524-94312	RESULT 1 PCT-USO0-35491-10 Sequence 10, Application PC/TUS0035491 Sequence 10, Application PC/TUS0035491 Sequence 10, Application PC/TUS0035491 Sequence 10, Application PC/TUS0035491 Sequence 10, Application David APPLICANT: Robertson, David TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND THERAPEDTIC METHODS RELATING THERETO TITLE OF INVENTION: DACKON DOCKET NO. 1242-27 PCT CURRENT APPLICATION NUMBER: PCT/US00/33491 CURRENT FILING DATE: 2000-12-28 PRIOR APPLICATION NUMBER: 60/175,456 PRIOR APPLICATION NUMBER: 60/173,682 PRIOR PLING DATE: 1999-12-29 NUMBER OF SEQ ID NOS: 40 SOFTWARE: PARENTIN VOIT 2.0 SEQ ID NO 10 TYPE: DANA	re 15; DB 1; Le 1. No. 2.8e+02; Ismatches 0;
504 42 506 25 506 27 506 38 507 13 507 13 511 61 511 61 511 61 512 81 513 25 513 25 514 25 515 26 516 26 517 61 518 61 519 61 51	PC/T David David NETIC NETIC AGNOS BER: 000-1 (R: 6 18: 6 9-12-	100.C 100.C 1100.C 115 15 15 15 10 T
	Opplication AATION: Cobertson, Stately, Ra SMYION: DI S	ORGANISM: Homo sapiens T-USO0-35491-10 Query Match Best Local Similarity 100.0%; Scoulatches 15; Conservative 0; Matches 15; Conservative 0; Matches 15; Conservative 10; Matches 15; Conservative 10; Matches 15; Conservative 10; Matches 10; Maplication US/09750609 GENERAL INFORMATION: APPLICANT: Robertson, David AppliCANT: Blakely, Randy D.
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Sequence 580, App Sequence 585, App Sequence 577, App Sequence 562, App Sequence 589, App Sequence 13666, Sequence 15770, App Sequence 15770, App Sequence 5920, App Sequence 5920, App Sequence 5920, App Sequence 192, App Sequence 238, App Sequence 238, App Sequence 238, App Sequence 4638, App Sequence 4638, App Sequence 410774, Sequence 410774, Sequence 19112, App Sequence 1164, App Sequence 1164, App Sequence 15783, App Sequence 1583, App Sequence 1583, App Sequence 1583, App Sequence 5238, App Sequence 175832, Sequence 1253, App Sequence	estanences soluentes solue	ezunenbes
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; TYPE: DNA; ORGANISM: Homo sapiens
PCT-US00-35491-5
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PCT-US00-35491-6/c
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Sequence 5, Application PC/TUS0035491

GENERAL INFORMATION:
GENERAL INFORMATION:
TYPLE GAPLICANT: Blakely, Randy D

TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEGUTIC METHODS RELATING THERETO

CURRENT APPLICATION NUMBER: PCT/US00/35491

CURRENT FILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATHLING VATE: 20

SEQ TON 5

LENGTH: 41
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO FILE REPERENCE: Attorney Docket No. 1242-27-2-2 CURRENT APPLICATION NUMBER: US/09/750,609
CURRENT FILING DATE: 2000-112-28
PRIOR PILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR PILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 10
LENGTH: 15
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APPLICANT: Robertson, David
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GRNETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION UNMER: US/60/173,682
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 10
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Pred. No. 2.8e+02;
Mismatches 0;
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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US-60-173-682-10
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TYPE: DNA
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RESULT 6

US-09-750-609-5

S Sequence 5, Application US/09750609

GENERAL INFORMATION:
APPLICANT: Blackly, Randy D.
TILE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TILE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27-2-2
CURRENT FILING DATE: 2000-112-28
PRIOR FILING DATE: 2000-111-28
PRIOR PLICATION NUMBER: 60/175,456
SPRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PALENTIN VEY: 2.0
SOFTWARE: PALENTIN VEY: 2.0
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APPLICANT: Blakely, Randy D.
APPLICANT: Blakely, Randy D.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO CURRENT APPLICATION NUMBER: PCT/USO0/35491
CURRENT APPLICATION NUMBER: 60/175,456
PRIOR APPLICATION NUMBER: 60/175,456
PRIOR APPLICATION NUMBER: 60/175,682
PRIOR APPLICATION NUMBER: 60/173,682
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
NUMBER: OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.0
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0;
    Score 15; DB 1;
Pred. No. 2.9e+02;
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; Pred. No. 2.9e+02;
0; Mismatches 0;
                                                   0; Mismatches
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100.08;
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Best Local Similarity 100.
Matches 15; Conservative
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; ORGANISM: Homo sapiens
PCT-US00-35491-6
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US-09-750-609-5
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APPLICANT: Byrum. Joseph R.
APPLICANT: Byrum. Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Dlants
FILE REFERENCE: 38-21(15367)C
CURRENT FPLIAG DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/306,349
PRIOR PILING DATE: 1999-05-10
PRIOR FILING DATE: 1999-05-10
SED ID NO 2932
LENGTH: 197
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APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERBURE: 38-21(15367)8
CURRENT APPLICATION NUMBER: US/09/306,349
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 53893
SEQ ID NO 2932
LENGTH: 197
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0; Mismatches 0;
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LOCATION: (1)..(197)
OTHER INFORMATION: unsure at all n locations
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CURRENT APPLICATION NUMBER: US/60/173,682 CURRENT FILING DATE: 1999-12-29 NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-960-481-2932; Application US/09960481; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2932, Application US/09306349; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-60-173-682-6
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Best Local Similarity
Matches 15; Conserv
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US-09-306-349-2932
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                                                                                                                                                                LENGTH: 41
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Sequence 6, Application US/09750609

GENERAL INFORMATION:
APPLICANT: BLAKELY, Randy D.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE REPERENCE: Attorney Docket No. 1242-27-2-2
CURRENT APPLICATION NUMBER: US/09/750,609
CURRENT FILING DATE: 2000-10-28
PRIOR PILING DATE: 2000-01-11
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN OF SEQ ID NOS: 40
SOFTWARE: PATENT
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APPLICANT: ROBERTON, David
APPLICANT: BLAKELY, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27
CURRENT APPLICATION NUMBER: U5/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
ELENGTH: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 15; DB 29; 100.0%; Pred. No. 2.9e+02;
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-60-173-682-5
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                           CTTCTCCCCTGTT
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US-60-173-682-5
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Length 197;

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APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuare, Laura L.
APPLICANT: Willahy, Sara J.
APPLICANT: Nughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS FILE REPRENCE: PD-1033 CIP
CURRENT APPLICATION NUMBER: US/09/540,229
CURRENT APPLICATION AUGUST 193582
SOFTWARE: PER Program
SSC ID NO 47840
LENGTH: 248
ENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: HUMAN BRAIN NUMBER OF SEQUENCES: 4483
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 248;
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SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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100.0%; Pred. No. 2.9e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00535318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: a, t, c, g, or other US-09-540-229-47840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/60/048,002
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Stuart, Susan G.
Ito, Laura Y.
Akerblom, Ingrid E.
Delegeane, Angelo M.
Naudhton, Rebecca E.
Klingler, Tod M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                              Delegeane, Angelo M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure LOCATION: 211
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US-60-048-002-2907
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                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: To, Laura I.
APPLICANT: Akerblom, Laura I degeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Ningler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
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0
                                                             Length 197;
                                                                                                      Indels
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APPLICATION NUMBER: US/09/076,667
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Pred. No. 2.9e+02;
                                                           Score 15; DB 36;
Pred. No. 2.9e+02;
                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
; OTHER INFORMATION: Clone ID: 701040886H1
US-09-960-481-2932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTATION NUMBER: 39,132
REFERRNCE/DOCKET NUMBER: PD-0370P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 845-0555
TELEPHONE: (415) 845-4166
INFORMATION FOR SEQ ID NO: 2907:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-540-229-47840
; Sequence 47840, Application US/09540229
                                                                                                                                                                                                                                                                                       Sequence 2907, Application US/09076667 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4483
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                 3 CCTTCTCCCCTGTT 17
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MEDIUM TYPE: Floppy
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MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 3268389H1
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US-09-076-667-2907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Score 15; DB 48; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4668 Application US/09637890 GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Shyjan, Andrew W.
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 248 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
MMEDIATE SOURCE:
CLONE: 3268389H1
US-60-048-002-2907
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6 US-10-240-453-46 5 US-09-724-676-25358 5 US-09-724-676-25359 6 US-09-724-676-25357 6 US-09-724-676-25357 8 Equence 5 US-09-724-676-25357 8 Equence 5 US-09-724-676-25357 8 Equence 6 US-09-724-676-25357 8 Equence 6 US-09-724-676-25356 8 US-09-724-676-31283 8 Equence 6 US-09-724-676-31283 8 Equence 7 US-09-724-676-31283 8 Equence 8 US-09-724-676-31283 8 Equence 9 US-09-724-676-31283 8 Equence 10 US-09-724-676-3133 8 Equence 10 US-09-7	6 US-10-203-138A-5496 Sequence 5
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Sequence Sequence Sequence Sequence Sequence
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Sequence 1672, Sequence 18518 Sequence 18518 Sequence 14, A Sequence 14, A Sequence 14, A Sequence 69, A Sequence 633, Sequence 633, Sequence 633, Sequence 25814, Sequence 25814, Sequence 25818 Sequence 25818 Sequence 25818 Sequence 25818 Sequence 25818 Sequence 25818 Sequence 18512 Sequence 18515 Sequence 25812 Sequence 25812	sednence of sednen
-724-676A-1672 Sequence -724-676A-18518 Sequence -724-676A-18518 Sequence -724-676A-18521 Sequence -724-676A-18521 Sequence -724-676A-18521 Sequence -724-676A-47372 Sequence -724-676A-47372 Sequence -724-676A-47372 Sequence -724-676A-3886 Sequence -724-676A-3886 Sequence -724-676A-3886 Sequence -724-676A-3886 Sequence -724-676A-3886 Sequence -724-676A-1853 Sequence -724-676A-25819 Sequence -724-676A-18512 Sequence -724-676A-18512 Sequence -724-676A-18512 Sequence -724-676A-18515 Sequence	US-09-724-676-6495 Sequence US-09-724-676-6495 Sequence US-09-992-643-269 Sequence US-09-992-643-269 Sequence US-10-131-813A-443 Sequence US-10-131-813A-443 Sequence US-10-131-824A-443 Sequence US-10-131-824A-443 Sequence US-10-127-825A-443 Sequence US-10-127-838A-443 Sequence US-10-127-843A-443 Sequence US-10-127-843A-443 Sequence US-10-127-843A-443 Sequence US-10-127-843A-443 Sequence US-10-128-864A-443 Sequence US-1
US-09-724-676A-1672 US-09-724-676-18518 US-09-724-676-18518 US-09-724-676-18518 US-09-724-676-18518 US-09-724-676-18521 US-09-724-676-18521 US-09-724-676-18521 US-09-724-676-18521 US-09-724-676-18521 US-09-724-676-1872 US-09-724-676-1872 US-09-724-676-1872 US-09-724-676-1873 US-09-724-676-1873 US-09-724-676-1873 US-09-724-676-1873 US-09-724-676-1874 US-	327 5 US-09-724-676-6495 Sequence (28-09-724-676-6495) Sequence (28-09-992-643-269) Sequence (28-09-992-643-269) Sequence (28-09-992-643-269) Sequence (28-09-131-813A-443) Sequence (28-10-131-813A-443) Sequence (28-1
187 5 US-09-724-676A-1672 Sequence 190 5 US-09-724-676A-18518 Sequence 190 5 US-09-724-676A-18518 Sequence 190 5 US-09-724-676-18518 Sequence 190 5 US-09-724-676-18521 Sequence 194 1 PCT-US02-32432-44 Sequence 192 5 US-09-724-676-18521 Sequence 192 5 US-09-724-676-47372 Sequence 193 10	3.3 1327 5 US-09-724-676-6495 Sequence 13.3 1325 5 US-09-98-733-269 Sequence 13.3 1325 5 US-09-98-733-269 Sequence 13.3 1332 5 US-09-98-733-269 Sequence 13.3 1332 6 US-10-131-813A-443 Sequence 13.3 1332 6 US-10-131-824A-443 Sequence 13.3 1332 6 US-10-131-824A-443 Sequence 13.3 1332 6 US-10-131-824A-443 Sequence 13.3 1332 6 US-10-127-824A-443 Sequence 13.3 1332 6 US-10-127-834A-443 Sequence 13.3 1332 6 US-10-128-684A-443 Sequence 13.3 1332 6 US-10-127-834A-443 Sequence 13.3 1332 6 US-10-127-834A-443 Sequence 13.3 1332 6 US-10-128-684A-443 Sequence 13.3 1332 6 US-10-128-684A-443 Sequence 13.3 1332 6 US-10-138-834A-443 Sequence 13.3 1332 6 US-10-138-834A-443 Sequence 13.3 1332 6 US-10-138-834A-443 Sequence 13.3 1332 6 US-10-138-844A-443 Sequence 13.3 1332 6 U
3.3 1187 5 US-09-724-676A-1672 Sequence 1190 5 US-09-724-676-18518 Sequence 1190 5 US-09-724-676-18518 Sequence 1190 5 US-09-724-676A-18518 Sequence 1193 5 US-09-724-676A-18518 Sequence 1193 5 US-09-724-676A-18521 Sequence 1194 1 PCT-US02-3342-44 Sequence 1202 5 US-09-724-676A-18521 Sequence 1202 5 US-09-724-676A-18521 Sequence 1202 5 US-09-724-676A-1872 Sequence 1202 5 US-09-724-676A-1872 Sequence 1202 5 US-09-724-676A-1873 Sequence 1202 5 US-09-724-676A-1888 Sequence 1202 5 US-09-724-676A-1888 Sequence 1202 5 US-09-724-676A-1888 Sequence 1202 5 US-09-724-676A-1888 Sequence 1202 5 US-09-724-676A-1889 Sequence 1203 5 US-09-724-676A-1889 Sequence 1209 5 US-09-724-676A-1889 Sequence 1209 5 US-09-724-676A-18819 Sequence 1208 5 US-09-724-676A-18	73.3 1327 5 US-09-724-676-6495 Sequence 73.3 1327 5 US-09-724-676-6495 Sequence 73.3 1332 5 US-09-982-643-269 Sequence 73.3 1332 6 US-09-982-643-269 Sequence 73.3 1332 6 US-10-131-813A-443 Sequence 73.3 1332 6 US-10-131-824A-443 Sequence 73.3 1332 6 US-10-127-824A-443 Sequence 73.3 1332 6 US-10-127-824A-443 Sequence 73.3 1332 6 US-10-127-824A-443 Sequence 73.3 1332 6 US-10-127-834A-443 Sequence 73.3 1332 6 US-10-127-824A-443 Sequence 73.3 1332 6 US-10-127-824A-443 Sequence 73.3

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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PALENTIN VET: 3.1
; SEQ ID NO 1036
; LENGTH: 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 15; DB 6; Length 2520; 100.0%; Pred. No. 7.2;
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US-09-620-607B-1245/C

Sequence 1245, Application US/09620607B

GENERAL INFORMATION:
APPLICANT: Nehls, Michael
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Ands, Arthur T.
TITLE OF INVENTION: Novel Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE OF INVENTION: Animals
CURRENT APPLICATION NUMBER: US/09/620,607B
CURRENT FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/144942
PRIOR APPLICATION NUMBER: US 60/144942
PRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 1848
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 248
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; Sequence 38339, Application US/09724676
; GENERAL INFORMATION
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT FILION NUMBER: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SEQ ID NO 38339
; LENGTH: 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:

NAME/KEY: misc_feature

LOCATION: (99)...(99)

USTHER INFORMATION: n equals a,t,g, or US-10-264-237-1036
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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                Sequence 14538, A Sequence 14509, A Sequence 14522, A Sequence 14522, A Sequence 24662, A Sequence 24662, A Sequence 14514, A Sequence 14514, A Sequence 14514, A Sequence 9011, Ap Sequence 14528, A Sequence 14528, A Sequence 15798, A Sequence 25798, A Sequence 25798, A Sequence 113, App Sequence 113, App Sequence 1051, A Sequence 10561, A Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.052.RG
CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NOS: 31681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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             US-09-724-676A-14538
US-09-724-676-14509
US-09-724-676-14520
US-09-724-676-14522
US-09-724-676-14522
US-09-724-676-14522
US-09-724-676-14514
US-09-724-676-14514
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US-09-724-676-14514
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US-09-724-676A-14528
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US-09-724-676A-14528
US-09-724-676A-15798
US-09-724-676A-15798
US-09-724-676A-15798
US-10-278-173-113
US-10-278-173-113
US-10-278-173-113
US-09-724-676-10551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13316, Application US/09513999C GENERAL INFORMATION:
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; Sequence 1036, Application US/10264237
GENERAL INFORMATION:
; APPLICANT: Birse et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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US-09-513-999C-13316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: k=g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                     NAME/KEY: misc_feature LOCATION: 298
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Matches 15; Conserv
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US-09-513-999C-13316/c
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Gaps

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0; Indels

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Gaps

; 0

Indels

Mismatches

Length 1030;

DB 5; 27;

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US-09-724-676-2247/C

Sequence 2247, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REPERENCE: 12181.4 Compugen

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 2247

LENGTH: 1509
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- US-09-724-676A-2247/C

| Sequence 2247, Application US/09724676A
| Sequence 2247, Application US/09724676A
| SEQUENCE 2247, Application US/09724676A
| TILLE OF INVENTION:
| APPLICANT: Compugen LTD
| TILLE OF INVENTION: Variants of alternative splicing
| FILE REFERENCE: 129181.4 Compugen
| CURRENT APPLICATION NUMBER: US/09/724,676A
| CURRENT FILING DATE: 2000-11-28
| SOFTWARE: PATENTION NOS: 97222
| SOFTWARE: PATENTION VERSION 3.2
| SEQUENTION OF SEQUENTIAL OF SE
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US-09-724-676-2234/c
; Sequence 2234, Application US/09724676
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100.0%;
                           NUMBER OF SEQ ID NOS: 97222
SOFWARE: Patentin version 3.2
SEQ ID NO 24274
LENGTH: 1030
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; ORGANISM: Homo sapiens
US-09-724-676A-24274
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; ORGANISM: Homo sapiens
US-09-724-676A-2247
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CURRENT FILING DATE:
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SERENAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INFORMATION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 38339
LENGTH: 908
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US-09-724-676A-24274/C
US-09-724-676A-24274, Application US/09724676A
; GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
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Sequence 24274, Application US/09724676
GENERAL INFORMATION:
APPLICAR: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNBER: US/09/724,676
CURRENT FILNG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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Live 0; Mismatches
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Best Local Similarity 100.
Matches 14; Conservative
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                           ; ORGANISM: Homo sapiens US-09-724-676-38339
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Matches 14; Conserv
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US-09-724-676A-38339
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; TYPE: DNA
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Sequence 2240, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FELIATON NUMBER: US/09/724,676A
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 2240
LENGTH: 1755
                                        US-09-724-676A-2221/C

Sequence 2221, Application US/09724676A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compagen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PatentIn version 3.2

SEQ ID NO 22211

LENGTH: 1712
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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iive 0; Mismatches
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Best Local Similarity 100.
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CORGANISM: Homo sapiens
US-09-724-676A-2240
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US-09-724-676-2240
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US-09-724-676A-2240/c
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US-09-724 e676-2221/C
Sequence 221, Application US/09724676
Sequence 221, Application US/09724676
Settle 221, Application US/09724676
SENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
CURRENT APPLICATION NUMBER: US/09/724,676
UNMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 2221
LENGTH: 1712
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            TITLE OF INVENTION: Variants of alternative splicing TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129/181.4 Compugen CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: PatentIn version 3.2 EEQ ID NO 2234 LENGTH: 1667
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iive 0; Mismatches (
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100.0%; Pred. No. 26;
Live 0; Mismatches
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Best Local Similarity 100.
Matches 14; Conservative
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US-09-724-676-2221
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CORGANISM: Homo sapiens
US-09-724-676A-2234
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CORGANISM: Homo sapiens
US-09-724-676-2234
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GENERAL INFORMATION:
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US-09-724-676A-2234/c
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